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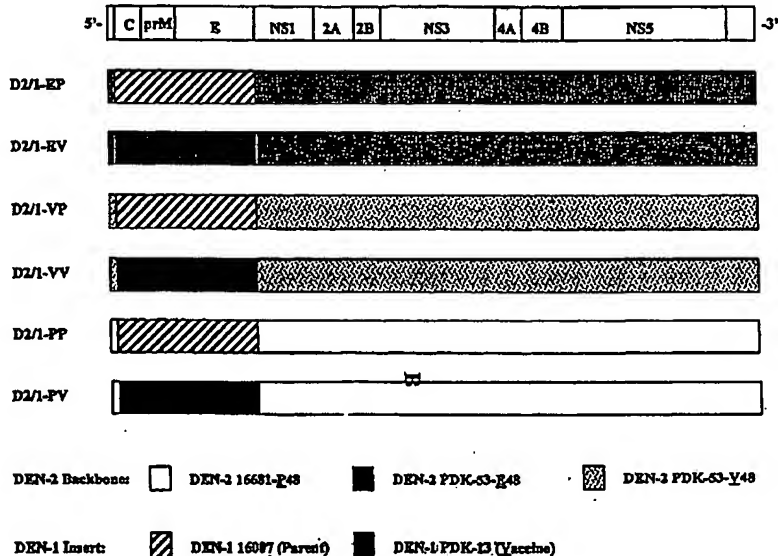
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(54) Title: **AVIRULENT, IMMUNOGENIC FLAVIVIRUS CHIMERAS**

(57) Abstract: Chimeric flaviviruses that are avirulent and immunogenic are provided. The chimeric viruses are constructed to contain amino acid mutations in the nonstructural proteins of a flavivirus. Chimeric viruses containing the attenuation-mutated nonstructural genes of the virus are used as a backbone into which the structural protein genes of a second flavivirus strain are inserted. These chimeric viruses elicit pronounced immunogenicity yet lack the accompanying clinical symptoms of viral disease. The attenuated chimeric viruses are effective as immunogens or vaccines and may be combined in a pharmaceutical composition to confer simultaneous immunity against several strains of pathogenic flaviviruses.

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AVIRULENT, IMMUNOGENIC FLAVIVIRUS CHIMERAS

This application claims priority to provisional application Serial No. 60/182,829, filed February 16, 2000, which is herein incorporated in its entirety.

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This invention was made by the Centers for Disease Control and Prevention, an agency of the United States Government. Therefore, the United States Government has certain rights in this invention.

10 **FIELD OF THE INVENTION**

The present invention relates to the fields of immunology and virology and more particularly to avirulent, immunogenic flavivirus chimeras for the production of immunogenic, live, attenuated flavivirus vaccines.

15

BACKGROUND OF THE INVENTION

Dengue viruses are mosquito-borne pathogens of the genus *Flavivirus* (family Flaviviridae). Four serotypes of dengue virus (often abbreviated "DEN") have been identified, including dengue-1, dengue-2, dengue-3 and dengue-4 (DEN-1 to DEN-4). The flavivirus genome is a single-stranded, positive-sense RNA approximately 11 kb in length, containing a 5'-noncoding region (5'NC); a coding region encoding the viral structural proteins; five nonstructural proteins, designated NS1, NS2A, NS2B, NS3, NS4A, NS4B, NS5; and a 3'-noncoding region (3'NC). The viral structural proteins include the capsid, premembrane/membrane and envelope. The structural and nonstructural proteins are translated as a single polyprotein. The polyprotein is then processed by cellular and viral proteases.

Transmitted by *Aedes aegypti* mosquitoes to humans in tropical and subtropical regions of the world, dengue viruses cause millions of cases of disease every year,

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ranging from dengue fever to the often fatal dengue hemorrhagic fever/dengue shock syndrome (DHF/DSS). Secondary infection of humans with a heterologous serotype of DEN virus may induce an immunopathological response and is considered a possible risk factor for DHF/DSS. Therefore, the need exists for development of a vaccine that
5 confers simultaneous protection against all dengue virus strains.

Since eradication of *Aedes aegypti* mosquitoes appears to be practically infeasible, development of safe, effective vaccines against all four serotypes of dengue virus is a World Health Organization priority. However, no approved, effective vaccine
10 against any of the dengue virus strains is currently available. It has been demonstrated that serial passage of wild-type flaviviruses in various cell cultures, such as primary dog kidney (PDK) cells, produces virus variants that have reduced virulence, retain immunogenicity and produce no untoward clinical symptoms.

15 Live, attenuated dengue viruses of all four serotypes have been developed at Mahidol University in Thailand by passaging the wild-type viruses in cell culture. These are currently the most promising live, attenuated vaccine candidates for immunization against dengue virus infection and/or disease. These vaccine candidates have been designated by a combination of their dengue serotype, the cell line through
20 which they were passaged and the number of times they were passaged. Thus, a dengue serotype 1 wild-type virus passaged in PDK cells 13 times is designated as DEN-1 PDK-13 virus(nucleotide sequence, SEQ ID NO:3; amino acid sequence, SEQ ID NO:4). The other vaccine candidates are DEN-2 PDK-53 (nucleotide sequence, SEQ ID NO:15; amino acid sequence, SEQ ID NO:16), DEN-3 PGMK-30/FRhL-3
25 (thirty passages in primary green monkey kidney cells, followed by three passages in fetal rhesus lung cells)(nucleotide sequence, SEQ ID NO:21; amino acid sequence, SEQ ID NO:22) and DEN-4 PDK-48 (nucleotide sequence, SEQ ID NO:25; amino acid sequence, SEQ ID NO:26). These four candidate vaccine viruses were derived by tissue culture passage of wild-type parental DEN-1 16007 (nucleotide sequence, SEQ
30 ID NO:1; amino acid sequence, SEQ ID NO:2), DEN-2 16681(nucleotide sequence,

SEQ ID NO:13; amino acid sequence, SEQ ID NO:14), DEN-3 16562 (nucleotide sequence, SEQ ID NO:19; amino acid sequence, SEQ ID NO:20) and DEN-4 1036 (nucleotide sequence, SEQ ID NO:23; amino acid sequence, SEQ ID NO:24) viruses, respectively.

5

Preliminary human clinical trials with these attenuated viruses have indicated that DEN-2 PDK-53 has the lowest infectious dose (50% minimal infectious dose of 5 plaque forming units or PFU) in humans, is strongly immunogenic, and produces no unacceptable clinical symptoms. The DEN-1 PDK-13, DEN-3 PGMK-30/FRhL-3 and
10 DEN-4 PDK-48 vaccine virus candidates have higher 50% minimal infectious doses of 10,000, 3500, and 150 PFU, respectively, in humans. The higher infectious doses required for the latter three vaccine candidates raises concerns regarding the relative efficacy of each serotype component in a tetravalent dengue virus vaccine. Although only one immunization with monovalent DEN-2 PDK-53 virus or DEN-4 PDK-48
15 virus was required to achieve 100% seroconversion in human subjects, a booster was needed to achieve the same seroconversion rate for DEN-1 PDK-13 and DEN-3 PGMK-30/FRhL-3 viruses, which have the two highest infectious doses for humans.

The DEN-2 PDK-53 virus vaccine candidate, henceforth abbreviated PDK-53,
20 has several measurable biological markers associated with attenuation, including temperature sensitivity, small plaque size, decreased replication in mosquito C6/36 cell culture, decreased replication in intact mosquitoes, loss of neurovirulence for suckling mice and decreased incidence of viremia in monkeys. Clinical trials of the candidate PDK-53 vaccine have demonstrated its safety and immunogenicity in humans.
25 Furthermore, the PDK-53 vaccine induces dengue virus-specific T-cell memory responses in human vaccine recipients.

Except for DEN-2 PDK-53 virus, the number and identity of the genetic mutations that accrued during multiple passages in cell culture and that are associated
30 with the attenuated phenotypes of the vaccine candidates are unknown. Neither the

relative contributions of such attenuation-associated mutations to the actual mechanism of attenuation, nor the potential for reverse mutations to revert any of the vaccine candidates to the virulent biological phenotype of the wild-type dengue virus are known for any of these four vaccine candidates. An understanding of the attenuation markers
5 of a vaccine candidate is critical for the prediction of its stability and safety.

Accordingly, there is a need for avirulent, yet immunogenic, dengue viruses to be used in the development of dengue virus vaccines to confer protection against one or more dengue virus serotypes. What would be ideal is a vaccine that would
10 simultaneously protect an individual against several virulent strains of this potentially dangerous family (Flaviviridae) of viruses. Therefore, a tetravalent vaccine that can be used to immunize an individual against all four dengue serotypes is particularly needed.

SUMMARY OF THE INVENTION

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Immunogenic flavivirus chimeras, a dengue-2 virus backbone for preparing the flavivirus chimeras and methods for producing the flavivirus chimeras are described. The immunogenic flavivirus chimeras are provided, alone or in combination, in a pharmaceutically acceptable carrier as immunogenic compositions to minimize, inhibit,
20 or immunize individuals against infection by one or more flaviviruses or flaviviral strains, particularly strains of the dengue virus serotypes DEN-1, DEN-2, DEN-3 and DEN-4. When combined, the immunogenic flavivirus chimeras may be used as multivalent vaccines to confer simultaneous protection against infection by more than one species or strain of flavivirus. Preferably, the flavivirus chimeras are combined in
25 an immunogenic composition useful as a tetravalent vaccine against the four known dengue virus serotypes. The nucleic acid sequence for each of the DEN-1, DEN-3 and DEN-4 viruses is also provided, for use as probes to detect dengue virus in a biological sample.

The avirulent, immunogenic flavivirus chimeras provided herein contain the nonstructural protein genes of the attenuated dengue-2 virus, or the equivalent thereof, and one or more of the structural protein genes or immunogenic portions thereof of the flavivirus against which immunogenicity is to be conferred. For example, the preferred
5 chimera contains the attenuated dengue-2 virus PDK-53 genome as the viral backbone, and the structural protein genes encoding capsid, premembrane/membrane, or envelope of the PDK-53 genome, or combinations thereof, are replaced with the corresponding structural protein genes from a flavivirus to be protected against, such as a different flavivirus or a different dengue virus serotype. The resulting viral chimera has the
10 functional properties of the attenuated dengue-2 virus and is therefore avirulent, but expresses antigenic epitopes of the structural gene products and is therefore immunogenic.

In another embodiment, the preferred chimera is a nucleic acid chimera
15 comprising a first nucleotide sequence encoding nonstructural proteins from an attenuated dengue-2 virus, and a second nucleotide sequence encoding a structural protein from a second flavivirus. In a further preferred embodiment, the attenuated dengue-2 virus is vaccine strain PDK-53. In a further preferred embodiment, the structural protein can be the C, prM or E protein of a flavivirus. Examples of
20 flaviviruses from which the structural protein may be selected include, but are not limited to, dengue-1 virus, dengue-2 virus, dengue-3 virus, dengue-4 virus, West Nile virus, Japanese encephalitis virus, St. Louis encephalitis virus, yellow fever virus and tick-borne encephalitis virus. In a further embodiment, the structural protein may be selected from non-flavivirus species that are closely related to the flaviviruses, such as
25 hepatitis C virus.

In evaluating the chimeric virus of the invention, it was unexpectedly discovered that the avirulence of the attenuated PDK-53 virus strain is attributable to the presence of specific amino acid substitution mutations in the nonstructural proteins
30 and a nucleotide substitution mutation in the 5' noncoding region. This nucleotide

substitution mutation occurs in the stem of a stem-loop structure that is conserved in all four dengue serotypes. In particular, a single mutation at NS1-53, a double mutation at NS1-53 and at 5'NC-57, a double mutation at NS1-53 and at NS3-250, and a triple mutation at NS1-53, at 5'NC-57 and at NS3-250, can provide the attenuated DEN-2 virus of the present invention.

Furthermore, the genome of any dengue-2 virus containing non-conservative amino acid substitutions at these loci can be used as the backbone in the avirulent chimeras described herein. Furthermore, other flavivirus genomes containing analogous mutations at the same loci, after amino acid sequence or nucleotide sequence alignment and stem structure analysis can also be used as the backbone structure and are defined herein as being equivalent to attenuating mutations of the dengue-2 PDK-53 genome.

The backbone, that region of the chimera that comprises the 5' and 3' noncoding regions and the region encoding the nonstructural proteins, can also contain further mutations to maintain stability of the avirulent phenotype and to reduce the possibility that the avirulent virus or chimera might revert back to the virulent wild-type virus. For example, a second mutation in the stem of the stem/loop structure in the 5' noncoding region will provide additional stability, if desired.

These chimeric viruses can comprise nucleotide and amino acid substitutions, deletions or insertions in their structural and nonstructural proteins in addition to those specifically described herein.

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The structural and nonstructural proteins of the invention are to be understood to include any protein comprising or any gene encoding the sequence of the complete protein, an epitope of the protein, or any fragment comprising, for example, two or more amino acid residues thereof.

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The present invention also provides a method for making the chimeric viruses of this invention using recombinant techniques, by inserting the required substitutions into the appropriate backbone genome.

5 The present invention also provides compositions comprising a pharmaceutically acceptable carrier and attenuated chimeric viruses of this invention which contain amino acid sequences derived from other dengue virus serotypes, other flavivirus species or other closely related species, such as hepatitis C virus. As an object of the invention, the amino acid sequences derived from other dengue virus
10 serotypes, other flavivirus species or other closely related species, such as hepatitis C virus, are expressed in a host, host cell or cell culture. As a further object of the invention, proteins or polypeptides comprising the amino acid sequences derived from other dengue virus serotypes, other flavivirus species or other closely-related species, can act as immunogens and, thus, be used to induce an immunogenic response against
15 other dengue virus serotypes, other flavivirus species or other closely related species.

The present invention also provides compositions comprising a pharmaceutically acceptable carrier, one or more attenuated chimeric viruses of this invention and further immunizing compositions. Examples of such further immunizing
20 compositions include, but are not be limited to, dengue virus vaccines, yellow fever virus vaccines, tick-borne encephalitis virus vaccines, Japanese encephalitis virus vaccines, West Nile virus vaccines, hepatitis C virus vaccines or other virus vaccines. Such vaccines may be live attenuated virus vaccines, killed virus vaccines, subunit vaccines, recombinant DNA vector vaccines or any combination thereof.
25

A distinct advantage of the current invention is that it provides for mixtures of attenuated flavivirus chimeras to be used as vaccines in order to impart immunity against several flavivirus species simultaneously.

Thus, an object of the current invention is to provide a virus chimera containing amino acid or nucleotide substitutions which retain immunogenicity of the virus while preventing any pathogenic effects of the virus.

5 Another object of the present invention is to provide nucleic acid chimeras comprising nucleotide sequence from an attenuated dengue-2 virus and nucleotide sequence from a second flavivirus, wherein the nucleotide sequence from the second flavivirus directs the synthesis of flavivirus antigens.

10 Another object of the present invention is to provide compositions for vaccines comprising more than one flavivirus species.

Another object of the present invention is to provide a method for making immunogenic or vaccine compositions using recombinant techniques by inserting the
15 required substitutions into an appropriate flavivirus genome.

Another object of the invention is to provide compositions and methods for imparting immunity against more than one flavivirus simultaneously.

20 Another object of the invention is to provide nucleic acid probes and primers for use in any of a number of rapid genetic tests that are diagnostic for each of the vaccine viruses of the current invention. This object of the invention may be embodied in polymerase chain reaction assays, hybridization assays or other nucleic acid sequence detection techniques known to the art. A particular embodiment of this object is an
25 automated PCR-based nucleic acid detection system.

These and other objects, features and advantages of the present invention will become apparent after review of the following detailed description of the disclosed embodiments and the appended claims.

30

BRIEF DESCRIPTION OF THE FIGURES

FIGURE 1 schematically shows the genomic organization of the chimeric DEN-2/DEN-1 viruses. Designations of the chimeras are based on the DEN-2 virus-specific infectious clone backbones and the structural genes (C-prM-E) insert of DEN-1 viruses. Underlined letters of the backbone and insert viruses are used in the designations. D2/1 indicates DEN-2/DEN-1 chimera; the first letter following the hyphen is the DEN-2 viral backbone, parent 16681 (P), PDK53-E (E), or PDK53-V (V); the last letter indicates the structural genes from the parental DEN-1 16007 (P) strain or its vaccine derivative, strain PDK-13 (V). The PDK53-E backbone contains three DEN-2 PDK-53 virus-specific amino acid mutations (NS1-53-Asp, NS2A-181-Phe, and NS4A-75-Ala) as well as the 5'NC-57 mutation of PDK-53 virus. The PDK53-V backbone contains these same PDK-53 virus-specific loci plus the additional PDK-53 virus-specific NS3-250-Val locus.

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FIGURES 2A and 2B show the growth characteristics of the chimeric DEN-2/DEN-1 viruses in LLC-MK₂ cells. Stippled bars indicate DEN-1 16007 virus and the chimeric viruses expressing the structural proteins of DEN-1 16007 virus. Bars with stripes indicate DEN-1 PDK-13 virus and the chimeric viruses expressing structural proteins of PDK-13 virus. Blank bars indicate the three DEN-2 backbone viruses derived from infectious clones of DEN-2 16681 virus (P48) and the two variants (PDK53-E and PDK53-V; E48 and V48, respectively). Figure 2A: Mean (\pm SD) plaque diameters. Values were calculated from ten individual plaques of each virus on day 10 after infection. pp: pinpoint-size plaques less than 1 mm. Figure 2B: Temperature sensitivity (*ts*) and peak titers of chimeric viruses on day 8 or 10 after infection. The *ts* scores were based on the reduction of the virus titers at 38.7°C versus those at 37°C (-, +, 2+ and 3+ indicate titer reduction of less than or equal to 60%, 61-90%, 91-99%, >99%, respectively, calculated from at least three experiments). The graph bar heights represent the log₁₀ titers of the viruses at 37°C. The multiplicity of infection (m.o.i.) was approximately 0.001 PFU/cell.

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FIGURE 3 shows the growth curves of DEN-1 16007, DEN-1 PDK-13, DEN-2 16681-P48, DEN-2 PDK53-E48, DEN-2 PDK53-V48 and chimeric DEN-2/DEN-1 viruses in C6/36 cells. Cells were infected at an approximate m.o.i. of 0.001 PFU/ml.

- 5 FIGURES 4A-C. Figure 4A: Mean plaque diameters \pm SD in millimeters (n=12) of DEN-2 16681, PDK-53 and recombinant 16681/PDK-53 viruses at nine days after infection in LLC-MK₂ cells. Figure 4B: Peak replication titers at 6-8 days after infection of LLC-MK₂ cells at a m.o.i. of approximately 0.001 PFU/cell in a single experiment. Temperature sensitivity (*ts*) scores for viruses grown at 37 °C or 38.7 °C
- 10 in LLC-MK₂ cells are shown above the graph bars for peak replication titers. Scores of (-), (+/-) and (+) indicate less than 81%, 81-89% and 90-97% reduction in viral titer, respectively, at 38.7 °C. Scores were determined at eight days after infection. Figure 4C: Average peak replication titers at 12 days after infection of C6/36 cells at a multiplicity of approximately 0.001 PFU/cell in two independent experiments.
- 15 Individual peak titers from the two experiments are indicated by vertical lines in each graph bar. The numerical designations for recombinant Px and Vx viruses (where x = 5'NC, NS1, and/or NS3 loci) indicate parental (P in virus designation) 16681 virus-specific loci engineered into the PDK-53 virus-specific infectious cDNA clone or reciprocal candidate PDK-53 vaccine (V in virus designation) virus-specific loci
- 20 engineered into the 16681 clone, respectively. Cognate viruses are indicated in all three graphs by graph bars of identical solid or cross-hatching pattern. The cognate for P5 virus is V13 virus, assuming that the viral phenotype is determined predominantly by the 5'NC-57, NS1-53 and NS3-250 loci. Both P5 and V13 viruses contain the 5'NC-57-C (16681), NS1-53-Asp (PDK-53) and NS3-250- Val (PDK-53) loci within the genetic
- 25 backgrounds of PDK-53 and 16681 viruses, respectively.

DETAILED DESCRIPTION OF THE INVENTION

The following description includes the best presently contemplated mode of carrying out the invention. This description is made for the purpose of illustrating the general principles of the inventions and should not be taken in a limiting sense.

Immunogenic flavivirus chimeras, a dengue-2 virus or dengue-2 virus equivalent backbone for preparing the flavivirus chimeras of this invention and methods for preparing the flavivirus chimeras are provided herein. The immunogenic flavivirus chimeras are useful, alone or in combination, in a pharmaceutically acceptable carrier as immunogenic compositions to minimize, inhibit, or immunize individuals against infection by one or more flaviviruses or flaviviral strains, particularly strains of the dengue virus serotypes DEN-1, DEN-2, DEN-3 and DEN-4. When combined, the immunogenic flavivirus chimeras may be used as a multivalent vaccine to confer simultaneous protection against infection. Preferably, the dengue virus chimeras are combined in an immunogenic composition useful as a tetravalent vaccine against the four known dengue virus serotypes.

Immunogenic flavivirus chimeras of the current invention are also useful, in combination with avirulent virus strains, in a pharmaceutically acceptable carrier, as immunogenic compositions to minimize, inhibit or immunize individuals against infection by multiple pathogenic species. For example, one or more of the immunogenic flavivirus chimeras of the current invention can be combined with avirulent virus serotypes of selected flaviviruses to provide a safe and effective tetravalent vaccine against the four known dengue virus serotypes. In a further embodiment, the flavivirus chimeras of the current invention may be combined with avirulent virus vaccines to provide a safe and effective vaccine against infection by multiple pathogenic species.

30

The present invention also provides compositions comprising a pharmaceutically acceptable carrier, one or more attenuated chimeric viruses of this invention and further immunizing compositions. Examples of such further immunizing compositions include, but are not be limited to, dengue virus vaccines, yellow fever
5 vaccines, tick-borne encephalitis vaccines, Japanese encephalitis vaccines, West Nile virus vaccines, hepatitis C virus vaccines or other virus vaccines. Such vaccines may be live attenuated virus vaccines, killed virus vaccines, subunit vaccines, recombinant DNA vector vaccines or any combination thereof.

10 The nucleic acid sequence for each of the DEN-1, DEN-3 and DEN-4 viruses is also provided for use as probes to detect dengue virus in a biological sample.

Chimeras of the present invention can comprise the backbone of the dengue-2 virus of an attenuated dengue-2 virus and further nucleotide sequences selected from
15 more than one dengue virus serotype, other flavivirus species, other closely related species, such as hepatitis C virus, or any combination thereof. These chimeras can be used to induce an immunogenic response against more than one species selected from the dengue virus serotypes, flavivirus species, other closely related species or any combination thereof.

20

In another embodiment, the preferred chimera is a nucleic acid chimera comprising a first nucleotide sequence encoding nonstructural proteins from an attenuated dengue-2 virus, and a second nucleotide sequence encoding a structural protein from a second flavivirus. In a further preferred embodiment, the attenuated
25 dengue-2 virus is vaccine strain PDK-53. In a further preferred embodiment, the structural protein can be the C protein of a flavivirus, the prM protein of a flavivirus, the E protein of a flavivirus, or any combination thereof. Examples of flaviviruses from which the structural protein may be selected include, but are not limited to, dengue-1 virus, dengue-2 virus, dengue-3 virus, dengue-4 virus, West Nile virus,
30 Japanese encephalitis virus, St. Louis encephalitis virus, yellow fever virus and tick-

borne encephalitis virus. In a further embodiment, the structural protein may be selected from non-flavivirus species that are closely related to the flaviviruses, such as hepatitis C virus.

5 The terms "a," "an" and "the" as used herein are defined to mean one or more and include the plural unless the context is inappropriate.

 The term "residue" is used herein to refer to an amino acid (D or L) or an amino acid mimetic that is incorporated into a peptide by an amide bond. As such, the amino
10 acid may be a naturally occurring amino acid or, unless otherwise limited, may encompass known analogs of natural amino acids that function in a manner similar to the naturally occurring amino acids (*i.e.*, amino acid mimetics). Moreover, an amide bond mimetic includes peptide backbone modifications well known to those skilled in the art.

15

 Furthermore, one of skill in the art will recognize that individual substitutions, deletions or additions in the amino acid sequence, or in the nucleotide sequence encoding for the amino acids, which alter, add or delete a single amino acid or a small percentage of amino acids (typically less than 5%, more typically less than 1%) in an
20 encoded sequence are conservatively modified variations, wherein the alterations result in the substitution of an amino acid with a chemically similar amino acid. Conservative substitution tables providing functionally similar amino acids are well known in the art. The following six groups each contain amino acids that are conservative substitutions for one another:

- 25 1) Alanine (A), Serine (S), Threonine (T);
 2) Aspartic acid (D), Glutamic acid (E);
 3) Asparagine (N), Glutamine (Q);
 4) Arginine (R), Lysine (K);
 5) Isoleucine (I), Leucine (L), Methionine (M), Valine (V); and
30 6) Phenylalanine (F), Tyrosine (Y), Tryptophan (W).

As used herein, the terms “virus chimera,” “chimeric virus,” “flavivirus chimera” and “chimeric flavivirus” means an infectious construct of the invention comprising a portion of the nucleotide sequence of a dengue-2 virus and further nucleotide sequence that is not from the same dengue-2 virus. Thus, examples of
5 further nucleotide sequence include, but are not limited to, sequences from dengue-1 virus, dengue-2 virus, dengue-3 virus, dengue-4 virus, West Nile virus, Japanese encephalitis virus, St. Louis encephalitis virus, tick-borne encephalitis virus, yellow fever virus and any combination thereof.

10 As used herein, “infectious construct” indicates a virus, a viral construct, a viral chimera, a nucleic acid derived from a virus or any portion thereof, which may be used to infect a cell.

As used herein, “nucleic acid chimera” means a construct of the invention
15 comprising nucleic acid comprising a portion of the nucleotide sequence of a dengue-2 virus and further nucleotide sequence that is not of the same origin as the nucleotide sequence of the dengue-2 virus. Correspondingly, any chimeric flavivirus or flavivirus chimera of the invention is to be recognized as an example of a nucleic acid chimera.

20 The structural and nonstructural proteins of the invention are to be understood to include any protein comprising or any gene encoding the sequence of the complete protein, an epitope of the protein, or any fragment comprising, for example, two or more amino acid residues thereof.

25 Nucleotide sequences of the RNA genome of the viruses and chimeras of the current invention are recited in the sequence listings in terms of DNA.

Unless defined otherwise, all technical and scientific terms used herein have the same meaning as commonly understood by one having ordinary skill in the art to which
30 this invention pertains. Although other materials and methods similar or equivalent to

those described herein can be used in the practice or testing of the present invention, the preferred methods and materials are now described.

Flavivirus Chimeras

5 Dengue virus types 1-4 (DEN-1 to DEN-4) are mosquito-borne flavivirus pathogens. The flavivirus genome contains a 5'-noncoding region (5'-NC), followed by a capsid protein (C) encoding region, followed by a premembrane/membrane protein (prM) encoding region, followed by an envelope protein (E) encoding region, followed by the region encoding the nonstructural proteins (NS1-NS2A-NS2B-NS3-NS4A-
10 NS4B-NS5) and finally a 3' noncoding region (3'NC). The viral structural proteins are C, prM and E, and the nonstructural proteins are NS1-NS5. The structural and nonstructural proteins are translated as a single polypeptide and processed by cellular and viral proteases.

15 The flavivirus chimeras of the invention are constructs formed by fusing non-structural protein genes from one type, or serotype, of dengue virus or virus species of the flaviviridae, with protein genes, for example, structural protein genes, from a different type, or serotype, of dengue virus or virus species of the flaviviridae. Alternatively, a flavivirus chimera of the invention is a construct formed by fusing non-
20 structural protein genes from one type, or serotype, of dengue virus or virus species of the flaviviridae, with further nucleotide sequences that direct the synthesis of polypeptides or proteins selected from other dengue virus serotypes or other viruses of the flaviviridae.

25 The avirulent, immunogenic flavivirus chimeras provided herein contain the nonstructural protein genes of the attenuated dengue-2 virus, or the equivalent thereof, and one or more of the structural protein genes, or antigenic portions thereof, of the flavivirus against which immunogenicity is to be conferred. Suitable flaviviruses include, but are not limited to those listed in Table 1.

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Other suitable flaviviruses for use in constructing the flavivirus chimeras of the invention are wild-type, virulent DEN-1 16007 (SEQ ID NO:1; SEQ ID NO:2), DEN-2 16681 (SEQ ID NO:13; SEQ ID NO:14), DEN-3 16562 (SEQ ID NO:19; SEQ ID NO:20) and DEN-4 1036 (SEQ ID NO:23; SEQ ID NO:24) and attenuated, vaccine-
5 strain DEN-1 PDK-13 (SEQ ID NO:3; SEQ ID NO:4), DEN-2 PDK-53 (SEQ ID NO:15; SEQ ID NO:16), DEN-3 PMK-30/FRhL-3 (SEQ ID NO:21; SEQ ID NO:22) and DEN-4 PDK-48 (SEQ ID NO:25; SEQ ID NO:26). Further suitable flaviviruses, or variants of the above listed flaviviruses, are described herein. Genetic differences between the DEN-1, DEN-2, DEN-3 and DEN-4 wild type/attenuated virus pairs are
10 shown in Tables 2-5 along with changes in the amino acid sequences encoded by the viral genomes.

The sequence listings for DEN-2 PDK-53 provided herein (SEQ ID NO:15; SEQ ID NO:16) correspond to the DEN-2 PDK-53-V variant, wherein genome
15 nucleotide position 5270 is mutated from an A to a T and amino acid position 1725 of the polyprotein or amino acid position 250 of the NS3 protein contains a valine residue. The DEN-2 PDK-53 variant without this nucleotide mutation, DEN-2 PDK-53-E, differs from PDK-53-V only in this one position. DEN-2 PDK-53-E has an A at nucleotide position 5270 and a glutamate at polyprotein amino acid position 1725, NS3
20 protein amino acid position 250 (Table 3).

The sequence listings for DEN-3 16562 provided herein (SEQ ID NO:21; SEQ ID NO:22) correspond to the variant wherein genome nucleotide position 1521 is a T and amino acid position 476 of the polyprotein or amino acid position 196 of the E
25 protein contain a leucine. A second variant, present in DEN-3 16562 cultures has a T at nucleotide position 1521 and amino acid position 476 of the polyprotein or amino acid position 196 of the E protein contain a serine (Table 4).

The sequence listings for DEN-4 PDK-48 (SEQ ID NO:25; SEQ ID NO:26)
30 correspond to the variant wherein genome nucleotide positions: 6957 is a T and amino

acid position 2286 of the polyprotein and amino acid position 44 of NS4B protein is a phenylalanine, 7546 is a T and amino acid position 2366 of the polyprotein and amino acid position 240 of NS4B protein is a valine, and 7623 is a T and amino acid position 2508 of the polyprotein and amino acid position 21 of NS5 protein is a tyrosine (Table 5).

Throughout the text, designations of the chimeras are based on the DEN-2 virus-specific infectious clone backbones and the structural genes (prM-E or C-prM-E) insert of other flaviviruses. Each designation begins with DEN-2 for the dengue-2 backbone, followed by the strain from which the structural genes are inserted. The particular backbone variant is reflected in the next letter. The particular DEN-2 backbone variant from which the chimera was constructed is indicated by the following letter placed after a hyphen, parent 16681 (P), PDK53-E (E), or PDK53-V (V); the last letter indicates the C-prM-E structural genes from the parental (P) strain or its vaccine derivative (V) or the prM-E structural genes from the parental (P1) or its vaccine derivative (V1). For example; DEN-2/1-VP (SEQ ID NO:5; SEQ ID NO:6) denotes the chimera comprising the attenuated DEN-2 PDK-53V backbone comprising a valine at NS3-250 and the C-prM-E genes from wild-type DEN-1 16007; DEN-2/1-VV (SEQ ID NO:7; SEQ ID NO:8) denotes the DEN-2 PDK-53V backbone with the vaccine strain of dengue-1, DEN-1 PDK-13; DEN-2/1-VP1 (SEQ ID NO:27; SEQ ID NO:28) denotes the DEN-2 PDK-53V backbone and the prM-E genes from wild-type DEN-1 16007; DEN-2/3-VP1 (SEQ ID NO:9; SEQ ID NO:10) denotes the DEN-2 PDK-53V backbone and the prM-E genes from wild-type DEN-3 16562; DEN-2/4-VP1 (SEQ ID NO:11; SEQ ID NO:12) denotes the DEN-2 PDK-53V backbone and the prM-E genes from wild-type DEN-4 1036; and DEN-2/WN-PP1 (SEQ ID NO:17; SEQ ID NO:18) denotes the DEN-2 16681 backbone and the prM-E genes from West Nile NY99. Other chimeras of the present invention, denoted in the same manner, are clearly defined herein by the disclosed sequences. For instance, DEN-2/1-PV is defined herein as consisting of the wild-type dengue-2 backbone, DEN-2 16681, and the C-prM-E genes of the vaccine strain of dengue-1, DEN-1 PDK-13.

The preferred chimera of the invention, for example, contains the attenuated dengue-2 virus PDK-53 genome as the viral backbone, in which the structural protein genes encoding C, prM and E proteins of the PDK-53 genome, or combinations thereof, are replaced with the corresponding structural protein genes from a flavivirus to be
5 protected against, such as a different flavivirus or a different dengue virus strain. Newly discovered flaviviruses or flavivirus pathogens can also be incorporated into the DEN-2 backbone. Genetic recombinations with related viruses such as hepatitis C virus (HCV) could also be used to produce the chimeras of this invention. The resulting viral chimera has the functional properties of the attenuated dengue-2 virus
10 and is therefore avirulent, but expresses antigenic epitopes of the structural gene products and is therefore immunogenic.

Nine nucleotide mutations between the genomes of the wild type DEN-2 16681 virus and two attenuated PDK-53 virus strains are identified herein (Table 3). Three of
15 these mutations are silent mutations in that they do not result in the production of an amino acid that differs from the amino acid in the same position in the wild type virus. The first mutation is a C-to-T (wild type-to-PDK-53) nucleotide mutation at genome nucleotide position 57 (nt 57) in the 5' noncoding region. The second mutation is a A-to-T mutation at genome nucleotide position 524, encoding the amino acid substitution
20 Asp-to-Val in the structural protein premembrane region, prM-29.

In the nonstructural protein regions, a Gly-to-Asp (wild type-to-PDK-53) mutation was discovered at nonstructural protein NS1-53 (genome nucleotide position 2579); a Leu-to-Phe (wild type-to-PDK-53) mutation was discovered at nonstructural
25 protein NS2A-181 (genome nucleotide position 4018); a Glu-to-Val (wild type-to-PDK-53) mutation was discovered at nonstructural protein NS3-250 (genome nucleotide position 5270); and a Gly-to-Ala mutation (wild type-to-PDK-53) was discovered at nonstructural protein NS4A-75 (genome nucleotide position 6599).

The attenuated PDK-53 virus strain has a mixed genotype at genome nt 5270. A significant portion (approximately 29%) of the virus population encodes the non-mutated NS3-250-Glu that is present in the wild type DEN-2 16681 virus rather than the NS3-250-Val mutation. As both genetic variants are avirulent, this mutation may not be necessary in an avirulent chimera.

It was unexpectedly discovered that the avirulence of the attenuated PDK-53 virus strain can be attributed to the presence of specific mutations in the nucleotide sequence encoding nonstructural proteins and in the 5' noncoding region (Example 5). In particular, a single mutation at NS1-53, a double mutation at NS1-53 and at 5'NC-57, a double mutation at NS1-53 and at NS3-250 and a triple mutation at NS1-53, at 5'NC-57 and at NS3-250, result in attenuation of the DEN-2 virus. Therefore, the genome of any dengue-2 virus containing such non-conservative amino acid substitutions or nucleotide substitutions at these loci can be used as the backbone in the avirulent chimeras described herein. The backbone can also contain further mutations to maintain stability of the avirulent phenotype and to reduce the possibility that the avirulent virus or chimera might revert back to the virulent wild-type virus. For example, a second mutation in the stem of the stem/loop structure in the 5' noncoding region will provide additional avirulent phenotype stability, if desired. The stem of the stem-loop structure is composed of nucleotide residues 11-16 (CUACGU) (SEQ ID NO:29) and nucleotide residues 56-61 (ACGUAG) (SEQ ID NO:30) of the dengue-2 virus RNA sense sequence, wherein the underlined nucleotide is C in wild-type DEN-2 16681 virus and U in PDK-53 virus. Mutations to this region disrupt potential secondary structures important for viral replication. In particular, mutations in the 5' noncoding region have the ability to disrupt the function of the positive-sense RNA strand and the function of the negative-sense strand during replication. A single mutation in this short (only 6 nucleotide residues in length) stem structure in both DEN and Venezuelan equine encephalitis viruses disrupts the formation of the hairpin structure (Kinney et al., *Virology* 67, 1269-1277, (1993)). Further mutations in this stem structure decrease the possibility of reversion at this locus, while maintaining

virus viability. Furthermore, flavivirus genomes containing an analogous stem structure that consists of short nucleotide sequences (stems consisting of 6 or more base pairs in the stem-loop structure) located in the 5' noncoding region and having one or more mutations in the stem structure may also be useful as the backbone structure of this invention.

Such mutations may be achieved by site-directed mutagenesis using techniques known to those skilled in the art. Furthermore, other flavivirus genomes containing analogous mutations at the same loci after amino acid sequence alignment, can be used as the backbone structure of the chimera of this invention and are defined herein as being equivalent to the dengue-2 PDK-53 genome. It will be understood by those skilled in the art that the virulence screening assays, as described herein and as are well known in the art, can be used to distinguish between virulent and avirulent backbone structures.

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Construction of Flavivirus Chimeras

The flavivirus chimeras described herein can be produced by splicing one or more of the structural protein genes of the flavivirus against which immunity is desired into a PDK-53 dengue virus genome backbone, or the equivalent thereof as described above, using recombinant engineering techniques well known to those skilled in the art to remove the corresponding PDK-53 gene and replace it with the desired gene. Alternatively, using the sequences provided in the sequence listing, the nucleic acid molecules encoding the flavivirus proteins may be synthesized using known nucleic acid synthesis techniques and inserted into an appropriate vector. Avirulent, immunogenic virus is therefore produced using recombinant engineering techniques known to those skilled in the art.

As mentioned above, the gene to be inserted into the backbone encodes a flavivirus structural protein. Preferably the flavivirus gene to be inserted is a gene encoding a C protein, a PrM protein and/or an E protein. The sequence inserted into

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the dengue-2 backbone can encode both the PrM and E structural proteins. The sequence inserted into the dengue-2 backbone can encode the C, prM and E structural proteins. The dengue virus backbone is the PDK-53 dengue-2 virus genome and includes either the spliced genes that encode the C, PrM and/or E structural proteins of dengue-1 (DEN-2/1), the spliced genes that encode the PrM and/or E structural proteins of dengue-3 (DEN-2/3), or the spliced genes encode the PrM and/or E structural proteins of dengue-4 (DEN-2/4). In a particular embodiment of this invention, the spliced gene that encodes the structural protein of dengue-3 virus directs the synthesis of an E protein that contains a leucine at amino acid position 345.

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In a particular embodiment, the chimera of this invention encodes the C structural protein of dengue-2 virus and directs the synthesis of a C protein that contains a serine at amino acid position 100 and comprises a spliced gene encoding the structural proteins of dengue-4 which directs the synthesis of an E protein that contains a leucine at amino acid position 447.

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In a further embodiment, the chimera of this invention encodes the C structural protein of dengue-2 virus and directs the synthesis of a C protein that contains a serine at amino acid position 100 and comprises a spliced gene encoding the structural proteins of dengue-4 which directs the synthesis of an E protein that contains a leucine at amino acid position 447 and a valine at amino acid position 364. The structural proteins described herein can be present as the only flavivirus structural protein or in any combination of flavivirus structural proteins in a viral chimera of this invention.

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The chimeras of this invention are engineered by recombination of full genome-length cDNA clones derived from both DEN-2 16681 wild type virus and either of the PDK-53 dengue-2 virus variants (-E or -V(SEQ ID NO:15)). The uncloned PDK-53 vaccine contains a mixture of two genotypic variants, designated herein as PDK53-E and PDK53-V. The PDK53-V variant contains all nine PDK-53 vaccine-specific nucleotide mutations, including the Glu-to-Val mutation at amino acid position NS3-

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250. The PDK53-E variant contains eight of the nine mutations of the PDK-53 vaccine and the NS3-250-Glu of the parental 16681 virus. Infectious cDNA clones are constructed for both variants, and viruses derived from both clones are attenuated in mice. The phenotypic markers of attenuation of DEN-2 PDK-53 virus include small
5 plaque size, temperature sensitivity (particularly in LLC-MK₂ cells), limited replication (particularly in C6/36 cells), attenuation for newborn mice (specifically loss of neurovirulence for suckling mice) and decreased incidence of viremia in monkeys. The chimeras that are useful as vaccine candidates are constructed in the genetic backgrounds of the two DEN-2 PDK-53 variants which all contain mutations in
10 nonstructural regions of the genome, including 5'NC-57 C-to-T (16681-to-PDK-53) in the 5' noncoding region, as well as mutations in the amino acid sequence of the nonstructural proteins, such as, for example, NS1-53 Gly-to-Asp and NS3-250 Glu-to-Val.

15 Suitable chimeric viruses or nucleic acid chimeras containing nucleotide sequences encoding structural proteins of other flaviviruses or dengue virus serotypes can be evaluated for usefulness as vaccines by screening them for the foregoing phenotypic markers of attenuation that indicate avirulence and by screening them for immunogenicity. Antigenicity and immunogenicity can be evaluated using *in vitro* or
20 *in vivo* reactivity with flavivirus antibodies or immunoreactive serum using routine screening procedures known to those skilled in the art.

Flavivirus Vaccines

The preferred chimeric viruses and nucleic acid chimeras provide live,
25 attenuated viruses useful as immunogens or vaccines. In a preferred embodiment, the chimeras exhibit high immunogenicity while at the same time producing no dangerous pathogenic or lethal effects.

Until now, an effective vaccine against all strains of dengue virus has been
30 unavailable. Individual live attenuated vaccine candidates for all four serotypes have

been developed by serial passage of wild-type viruses in primary dog kidney (PDK) cells or other cell types. As described above, the PDK-53 virus is a useful dengue vaccine candidate. However, a vaccine derived from PDK-53 would only provide immunity against the DEN-2 serotype.

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To prevent the possible occurrence of DHF/DSS in patients vaccinated against only one serotype of dengue virus, a tetravalent vaccine is needed to provide simultaneous immunity for all four serotypes of the virus. A tetravalent vaccine is produced by combining dengue-2 PDK-53 with the dengue-2/1, dengue-2/3, and
10 dengue-2/4 chimeras described above in a suitable pharmaceutical carrier for administration as a multivalent vaccine.

The chimeric viruses or nucleic acid chimeras of this invention can comprise the structural genes of either wild-type or attenuated virus in a virulent or an attenuated
15 DEN-2 virus backbone. For example, the chimera may express the structural protein genes of wild-type DEN-1 16007 virus or its candidate PDK-13 vaccine derivative in either of the DEN-2 PDK-53 backgrounds.

As described in Example 1, all of the chimeric DEN-2/1 viruses containing the
20 C, prM and E proteins of either DEN-1 16007 virus (DEN-2/1-EP and -VP chimeras) or PDK-13 virus (DEN-2/1-EV and -VV (SEQ ID NO:7) chimeras) in the backbones of DEN-2 PDK-53 retain all of the phenotypic attenuation markers of the DEN-2 PDK-53 virus. The chimeric DEN-2/1-EP and -VP(SEQ ID NO:5) viruses, which contain the C, prM and E proteins of DEN-1 16007 virus are more genetically stable after passing in
25 cell culture than the DEN-2/1-EV and -VV viruses. The immunogenicity of the chimeric viruses expressing the structural proteins of DEN-1 16007 virus was higher as compared with the neutralizing antibody titers elicited by the PDK-13 vaccine virus and the chimeras expressing the structural proteins of the PDK-13 virus. Thus, the chimeric DEN-2/1-EP and -VP viruses, which express the structural genes of wild-type DEN-1
30 16007 virus within the genetic background of the two DEN-2 PDK-53 variants, are

potential DEN-1 vaccine candidates that are superior to the candidate PDK-13 vaccine. These two chimeras replicate well in LLC-MK₂ cells and retain the attenuation markers associated with DEN-2 PDK-53 virus, including small plaque size, temperature sensitivity, restricted replication in mosquito cells and attenuation for mice. They are at least as immunogenic as wild-type DEN-1 16007 virus in mice.

Other examples, such as DEN-2/3 and DEN-2/4 chimeras, in Examples 2-4, also showed that chimeric viruses containing structural protein genes from wild-type DEN-3 or DEN-4 virus within the DEN-2 PDK-53 backbones, are suitable vaccine candidates which retain all of the attenuated phenotypic markers of the DEN-2 PDK-53 viruses (Table 14), while providing immunogenicity against DEN-3 or DEN-4 virus. The strategy described herein of using a genetic background that contains the determinants of attenuation in nonstructural regions of the genome to express the structural protein genes of heterologous viruses has lead to development of live, attenuated flavivirus vaccine candidates that express wild-type structural protein genes of optimal immunogenicity. Thus, vaccine candidates for immunogenic variants of multiple flaviviral pathogens can be designed.

Viruses used in the chimeras described herein are typically grown using techniques known in the art. Virus plaque titrations are then performed and plaques counted in order to assess the viability and phenotypic characteristics of the growing cultures. Wild type viruses are passaged through cultured cell lines to derive attenuated candidate starting materials.

Chimeric infectious clones are constructed from the various dengue serotype clones available. The cloning of virus-specific cDNA fragments can also be accomplished, if desired. The cDNA fragments containing the structural protein or nonstructural protein genes are amplified by reverse transcriptase-polymerase chain reaction (RT-PCR) from dengue virus RNA with various primers. Amplified fragments are cloned into the cleavage sites of other intermediate clones. Intermediate, chimeric

dengue virus clones are then sequenced to verify the accuracy of the inserted dengue virus-specific cDNA.

Full genome-length chimeric plasmids constructed by inserting the structural
5 protein or nonstructural protein gene region of dengue serotype viruses into vectors are obtainable using recombinant techniques well known to those skilled in the art.

Nucleotide and Amino Acid Analysis

The nucleotide sequence for DEN-2 16681 and corresponding PDK-53-V are
10 provided in SEQ ID NO:13 and SEQ ID NO:15, respectively. Amino acid sequences for DEN-2 16681 and corresponding PDK-53-V are provided in SEQ ID NO:14 and SEQ ID NO:16. The -E variant of PDK-53, which varies from PDK-53-V at nucleotide position 5270 and amino acid position 1725 of the polyprotein is further described in Table 3. A comparison of the critical nucleotide and amino acid
15 substitutions that have been discovered between the parent strain and the attenuated virus is shown in Table 3. The sequence of the DEN-2 cDNA amplicons was amplified from DEN-2 viral genomic RNA by reverse transcriptase-polymerase chain reaction (RT-PCR).

20 Unlike PDK-53, which contains no amino acid mutations in the E protein relative to wild type dengue-2 virus, the Mahidol DEN-1, DEN-3 and DEN-4 attenuated viruses all have amino acid mutations in the E protein (Tables 2, 4 & 5). The wild-type DEN-3 16562 listed in the sequence listing (nucleotide sequence, SEQ ID NO:19; amino acid sequence, SEQ ID NO:20) was shown to comprise traces of a
25 variant comprising a T at nucleotide position 1521 which directs incorporation of a leucine at polypeptide position 476, amino acid residue position 476 of the E protein.

Each of the latter three viruses possess a Glu-to-Lys (parent-to-vaccine)
mutation in the E protein, although the mutation is located at a different amino acid
30 residue in the E protein. This substitution causes a shift from a negatively charged

amino acid to a positively charged one. The Glu-to-Lys substitution in the E protein of DEN-4 vaccine virus was the only mutation present in the E protein, while the E proteins of DEN-1 and DEN-3 vaccine viruses had five and three amino acid mutations, respectively.

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The NS1-53 mutation in the DEN-2 PDK-53 vaccine virus is significant for the attenuated phenotype of this virus, because the NS1-53-Gly of the DEN-2 16681 virus is conserved in nearly all flaviviruses, including the tick-borne viruses, sequenced to date. The Mahidol DEN-4 vaccine virus also contains an amino acid mutation in the NS1 protein at position 253. This locus, which is a Gln-to-His mutation in DEN-4 PDK-48 vaccine virus is Gln in all four wild serotypes of dengue virus. This Gln residue is unique to the dengue viruses within the flavivirus genus. The NS1 protein is a glycoprotein that is secreted from flavivirus-infected cells. It is present on the surface of the infected cell and NS1-specific antibodies are present in the serum of virus-infected individuals. Protection of animals immunized with NS1 protein or passively with NS1-specific antibody has been reported. The NS1 protein appears to participate in early viral RNA replication.

The mutations that occurred in the NS2A, NS2B, NS4A, and NS4B proteins of the DEN-1, -2, -3 and -4 attenuated strains were all conservative in nature. The NS4A-75 and NS4A-95 mutations of DEN-2 and DEN-4 vaccine viruses, respectively, occurred at sites of amino acid conservation among dengue viruses, but not among flaviviruses in general.

The flaviviral NS3 protein possesses at least two recognized functions: the viral proteinase and RNA helicase/NTPase. The 698-aa long (DEN-2 virus) NS3 protein contains an amino-terminal serine protease domain (NS3-51-His, -75-Asp, -135-Ser catalytic triad) that is followed by sequence motifs for RNA helicase/NTPase functions (NS3-196-GAGKT (SEQ ID NO:147), -284-DEAH, -459-GRIGR (SEQ ID NO:148)). None of the mutations in the NS3 proteins of DEN-1, DEN-2, or DEN-3 virus occurred

within a recognized motif. The NS3-510 Tyr-to-Phe mutation in DEN-1 PDK-13 virus was conservative. Since the wild-type DEN-2, -3 and -4 viruses contain Phe at this position, it is unlikely that the Tyr-to-Phe mutation plays a role in the attenuation of DEN-1 virus. The NS3-182 Glu-to-Lys mutation in DEN-1 PDK-13 virus occurred at a position that is conserved as Asp or Glu in most mosquito-borne flaviviruses and it may play some role in attenuation. This mutation was located 15 amino acid residues upstream of the GAGKT (SEQ ID NO:147) helicase motif. As noted in previous reports, the NS3-250-Glu in DEN-2 16681 virus is conserved in all mosquito-borne flaviviruses except for yellow fever virus.

10

Method of Administration

The viral chimeras described herein are individually or jointly combined with a pharmaceutically acceptable carrier or vehicle for administration as an immunogen or vaccine to humans or animals. The terms "pharmaceutically acceptable carrier" or "pharmaceutically acceptable vehicle" are used herein to mean any composition or compound including, but not limited to, water or saline, a gel, salve, solvent, diluent, fluid ointment base, liposome, micelle, giant micelle, and the like, which is suitable for use in contact with living animal or human tissue without causing adverse physiological responses, and which does not interact with the other components of the composition in a deleterious manner.

The immunogenic or vaccine formulations may be conveniently presented in viral PFU unit dosage form and prepared by using conventional pharmaceutical techniques. Such techniques include the step of bringing into association the active ingredient and the pharmaceutical carrier(s) or excipient(s). In general, the formulations are prepared by uniformly and intimately bringing into association the active ingredient with liquid carriers. Formulations suitable for parenteral administration include aqueous and non-aqueous sterile injection solutions which may contain anti-oxidants, buffers, bacteriostats and solutes which render the formulation isotonic with the blood of the intended recipient, and aqueous and non-aqueous sterile suspensions which may

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include suspending agents and thickening agents. The formulations may be presented in unit-dose or multi-dose containers, for example, sealed ampoules and vials, and may be stored in a freeze-dried (lyophilized) condition requiring only the addition of the sterile liquid carrier, for example, water for injections, immediately prior to use.

- 5 Extemporaneous injection solutions and suspensions may be prepared from sterile powders, granules and tablets commonly used by one of ordinary skill in the art.

Preferred unit dosage formulations are those containing a dose or unit, or an appropriate fraction thereof, of the administered ingredient. It should be understood that
10 in addition to the ingredients particularly mentioned above, the formulations of the present invention may include other agents commonly used by one of ordinary skill in the art.

The immunogenic or vaccine composition may be administered through
15 different routes, such as oral or parenteral, including, but not limited to, buccal and sublingual, rectal, parenteral, aerosol, nasal, intramuscular, subcutaneous, intradermal, and topical. The composition may be administered in different forms, including, but not limited to, solutions, emulsions and suspensions, microspheres, particles, microparticles, nanoparticles and liposomes. It is expected that from about 1 to about 5
20 doses may be required per immunization regimen. Initial doses may range from about 100 to about 50,000 PFU, with a preferred dosage range of about 500 to about 20,000 PFU, a more preferred dosage range of from about 1000 to about 12,000 PFU and a most preferred dosage range of about 1000 to about 4000 PFU. Booster injections may range in dosage from about 100 to about 20,000 PFU, with a preferred dosage range of
25 about 500 to about 15,000, a more preferred dosage range of about 500 to about 10,000 PFU, and a most preferred dosage range of about 1000 to about 5000 PFU. For example, the volume of administration will vary depending on the route of administration. Intramuscular injections may range in volume from about 0.1 ml to 1.0 ml.

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The composition may be stored at temperatures of from about -100°C to about 4°C. The composition may also be stored in a lyophilized state at different temperatures including room temperature. The composition may be sterilized through conventional means known to one of ordinary skill in the art. Such means include, but are not limited to, filtration. The composition may also be combined with bacteriostatic agents, such as thimerosal, to inhibit bacterial growth.

Administration Schedule

The immunogenic or vaccine composition described herein may be administered to humans, especially individuals traveling to regions where dengue virus infection is present, and also to inhabitants of those regions. The optimal time for administration of the composition is about one to three months before the initial infection. However, the composition may also be administered after initial infection to ameliorate disease progression, or after initial infection to treat the disease.

15

Adjuvants

A variety of adjuvants known to one of ordinary skill in the art may be administered in conjunction with the chimeric virus in the immunogen or vaccine composition of this invention. Such adjuvants include, but are not limited to, the following: polymers, co-polymers such as polyoxyethylene-polyoxypropylene copolymers, including block co-polymers, polymer P1005, Freund's complete adjuvant (for animals), Freund's incomplete adjuvant; sorbitan monooleate, squalene, CRL-8300 adjuvant, alum, QS 21, muramyl dipeptide, CpG oligonucleotide motifs and combinations of CpG oligonucleotide motifs, trehalose, bacterial extracts, including mycobacterial extracts, detoxified endotoxins, membrane lipids, or combinations thereof.

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Nucleic Acid Sequences

Nucleic acid sequences of the DEN-1 16007 (SEQ ID NO:1), DEN-1 PDK-13 (SEQ ID NO:3), DEN-2 16681 (SEQ ID NO:13), DEN-2 PDK-53 (SEQ ID NO:15), DEN-3 16562 (SEQ ID NO:19), DEN-3 PGMK-30/FRhL-3 (SEQ ID NO:21), DEN-4 1036 (SEQ ID NO:23) and DEN-4 PDK-13 (SEQ ID NO:25) viruses are useful for designing nucleic acid probes and primers for the detection of dengue virus in a sample or specimen with high sensitivity and specificity. Probes or primers corresponding to each viral subtype can be used to detect the presence of DEN-1 virus, DEN-3 virus and DEN-4 virus, respectively, to detect dengue virus infection in general in the sample, to diagnose infection with dengue virus, to distinguish between the various dengue virus subtypes, to quantify the amount of dengue virus in the sample, or to monitor the progress of therapies used to treat a dengue virus infection. The nucleic acid and corresponding amino acid sequences are also useful as laboratory research tools to study the organisms and the diseases and to develop therapies and treatments for the diseases.

Nucleic acid probes selectively hybridize with nucleic acid molecules encoding the DEN-1, DEN-3 and DEN-4 viruses or complementary sequences thereof. By “selective” or “selectively” is meant a sequence which does not hybridize with other nucleic acids to prevent adequate detection of the dengue virus. Therefore, in the design of hybridizing nucleic acids, selectivity will depend upon the other components present in a sample. The hybridizing nucleic acid should have at least 70% complementarity with the segment of the nucleic acid to which it hybridizes. As used herein to describe nucleic acids, the term “selectively hybridizes” excludes the occasional randomly hybridizing nucleic acids, and thus, has the same meaning as “specifically hybridizing.” The selectively hybridizing nucleic acid of this invention can have at least 70%, 80%, 85%, 90%, 95%, 97%, 98%, and 99% complementarity with the segment of the sequence to which it hybridizes, preferably 85% or more.

The present invention also contemplates sequences, probes and primers which selectively hybridize to the encoding nucleic acid or the complementary, or opposite, strand of the nucleic acid. Specific hybridization with nucleic acid can occur with minor modifications or substitutions in the nucleic acid, so long as functional species-specific hybridization capability is maintained. By "probe" is meant nucleic acid sequences that can be used as probes or primers for selective hybridization with complementary nucleic acid sequences for their detection or amplification, which probes can vary in length from about 5 to 100 nucleotides, or preferably from about 10 to 50 nucleotides, or most preferably about 18-24 nucleotides. Therefore, the terms "probe" or "probes" as used herein are defined to include "primers." Isolated nucleic acids are provided herein that selectively hybridize with the species-specific nucleic acids under stringent conditions and should have at least five nucleotides complementary to the sequence of interest as described in Molecular Cloning: A Laboratory Manual, 2nd Ed., Sambrook, Fritsch and Maniatis, Cold Spring Harbor Laboratory, Cold Spring Harbor, NY, (1989).

If used as primers, the composition preferably includes at least two nucleic acid molecules which hybridize to different regions of the target molecule so as to amplify a desired region. Depending on the length of the probe or primer, the target region can range between 70% complementary bases and full complementarity and still hybridize under stringent conditions. For example, for the purpose of detecting the presence of the dengue virus, the degree of complementarity between the hybridizing nucleic acid (probe or primer) and the sequence to which it hybridizes is at least enough to distinguish hybridization with a nucleic acid from other organisms.

The nucleic acid sequences encoding the DEN-1, DEN-3 or DEN-4 virus can be inserted into a vector, such as a plasmid, and recombinantly expressed in a living organism to produce recombinant dengue virus peptides and/or polypeptides.

Nucleic Acid Detection Methods

A rapid genetic test that is diagnostic for each of the vaccine viruses described herein is provided by the current invention. This embodiment of the invention enhances analyses of viruses isolated from the serum of vaccinated humans who
5 developed a viremia, as well as enhancing characterization of viremia in nonhuman primates immunized with the Mahidol candidate vaccine viruses.

As provided in the complete nucleotide sequences of the wild-type parental and vaccine strains, and in the primer sequences provided in Table 16, the current invention
10 comprises viruses specific probes and primers to detect one or more of the mutations that have been identified in the genome of each vaccine virus. Specific detection of two or more virus specific loci allows specific identification of the particular vaccine circulating in the serum of a vaccinee. Examples of such probes specifically designed to allow detection of each of the DEN-1, DEN-2, DEN-3 and DEN-4 vaccine virus-
15 specific loci in a TaqMan assay are provided in Table 16.

These sequences include a diagnostic TaqMan probe that serves to report the detection of the cDNA amplicon amplified from the viral genomic RNA template by using a reverse-transcriptase/polymerase chain reaction (RT/PCR), as well as the
20 forward (F in Table 16) and reverse (R in Table 16) amplimers that are designed to amplify the cDNA amplicon, as described below. In certain instances, one of the amplimers has been designed to contain a vaccine virus-specific mutation (underlined residues in Table 16) at the 3'-terminal end of the amplimer, which effectively makes the test even more specific for the vaccine strain because extension of the primer at the
25 target site, and consequently amplification, will occur only if the viral RNA template contains that specific mutation. The probes and primers listed in Table 15 and Table 16 serve as examples of useful diagnostic sequences and are not intended to limit the design or scope of other probe and amplimer sequences that might be designed to detect the Mahidol vaccine virus-specific genetic mutations.

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A recently developed, automated PCR-based nucleic acid sequence detection system is the TaqMan assay (Applied Biosystems), which is becoming widely used in diagnostic laboratories. The TaqMan assay is a highly specific and sensitive assay that permits automated, real time visualization and quantitation of PCR-generated
5 amplicons from a sample nucleic acid template. TaqMan can determine the presence or absence of a specific sequence. In this assay, a forward and a reverse primer are designed to anneal upstream and downstream of the target mutation site, respectively. A specific detector probe, which is designed to have a melting temperature of about 10°C higher than either of the amplimers and containing the vaccine virus-specific
10 nucleotide mutation or its complement (depending on the strand of RT/PCR amplicon that is being detected), constitutes the third primer component of this assay.

The probe is a fluorescent detector or reporter oligonucleotide that contains a 5'-reporter dye and a 3'-quencher dye. The 5' end of the nucleotide is linked to one of a
15 number of different fluorescent reporter dyes, such as FAM (6-carboxyfluorescein) or TET (tetrachloro-6-carboxyfluorescein). At the 3'-end of the probe, the quenching dye TAMRA (6-carboxytetramethylrhodamine) is attached via a linker. The quenching dye suppresses the fluorescence of the reporter dye in the intact probe, where both dyes are in close proximity. If the probe-specific target sequence is present in the RT/PCR
20 amplicon, the probe will anneal between the forward and reverse primer sites in the amplicon. If the probe hybridizes to the target sequence, the 5'-3' nuclease activity of AmpliTaq Gold DNA polymerase (Applied Biosystems) cleaves the probe between the reporter dye and the quencher dye. The polymerase will not digest free probe. Because the polymerase displaces the probe, polymerization and PCR amplification continue.
25 Once separated from the quencher dye, the reporter dye produces a fluorescence that is measured by the ABI PRISM Sequence Detection System. If the probe-specific target sequence is present in the amplicon, the level of fluorescence increases with, and is automatically measured at, each amplifying PCR cycle.

A probe designed to specifically detect a mutated locus in one of the Mahidol vaccine viral genomes will contain the vaccine-specific nucleotide in the middle of the probe. This probe will result in detectable fluorescence in the TaqMan assay if the viral RNA template is vaccine virus-specific. However, genomic RNA templates from wild-type DEN viruses will have decreased efficiency of probe hybridization because of the
5 type DEN viruses will have decreased efficiency of probe hybridization because of the single nucleotide mismatch (in the case of the parental viruses DEN viruses) or possibly more than one mismatch (as may occur in other wild-type DEN viruses) and will not result in significant fluorescence. The DNA polymerase is more likely to displace a mismatched probe from the RT/PCR amplicon template than to cleave the
10 mismatched probe to release the reporter dye (TaqMan Allelic Discrimination assay, Applied Biosystems).

A more recently developed strategy for diagnostic genetic testing makes use of molecular beacons (Tyagi and Kramer, *Nature Biotechnology* 14:303-308(1996)). The
15 molecular beacon strategy also utilizes primers for RT/PCR amplification of amplicons, and detection of a specific sequence within the amplicon by a probe containing reporter and quencher dyes at the probe termini. In this assay, the probe forms a stem-loop structure. The 5'- and 3'- terminal reporter dye and quencher dye, respectively, are located at the termini of the short stem structure, which brings the quencher dye in
20 close juxtaposition with the reporter dye. The stem-structure is melted during the denaturation step of the RT/PCR assay. If the target viral RNA contains the target sequence and is amplified by the forward and reverse amplimers, the opened loop of the probed hybridizes to the target sequence during the annealing step of the cycle. When the probe is annealed to either strand of the amplicon template, the quencher and
25 reporter dyes are separated, and the fluorescence of the reporter dye is detected. This is a real-time identification and quantitation assay that is very similar to the TaqMan assay. The molecular beacons assay employs quencher and reporter dyes that differ from those used in the TaqMan assay.

The present invention is further illustrated by the following non-limiting examples, which are not to be construed in any way as imposing limitations upon the scope thereof. On the contrary, it is to be clearly understood that resort may be had to various other embodiments, modifications, and equivalents thereof which, after reading
5 the description herein, may suggest themselves to those skilled in the art without departing from the spirit of the present invention or the scope of the appended claims.

Example 1

Preparation of a Chimeric Dengue-1 Vaccine: PDK-53/Dengue-1

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Viruses and cell cultures

Wild-type DEN-1 16007 and DEN-2 16681 viruses were available in the virus collection at the Centers for Disease Control and Prevention (Atlanta, GA). DEN-1 16007 virus was recovered from the serum of a patient with DHF/DSS in 1964 in
15 Thailand. The virus was isolated following three passages in grivet monkey kidney BS-C-1 cells and one passage in LLC-MK₂ cells, passaged twice in *Toxorhynchites amboinensis* mosquitoes, and then passaged in primary dog kidney (PDK) cells at the Center for Vaccine Development, Mahidol University, Thailand, to derive the candidate DEN-1 PDK-13 vaccine virus (Yoksan et al., "Dengue virus vaccine development:
20 study on biological markers of uncloned dengue 1-4 viruses serially passaged in primary kidney cells," pp. 35-38, In Arbovirus research in Australia, Proceedings of the Fourth Symposium, CSIRO/QIMR, Brisbane, Australia (1986); Bhamarapravati & Sutee, *Vaccine* 18: 44-47 (2000)). A single LLC-MK₂ passage of this candidate vaccine virus (lot March 10, 1989) was used, unless otherwise mentioned. Following
25 the aforementioned mosquito passages, the 16007 virus was passaged once in LLC-MK₂ cells for use.

Viruses were grown in LLC-MK₂ and C6/36 cells in Dulbecco's modified minimal essential medium (DMEM) containing penicillin/streptomycin and 5% fetal
30 bovine serum (FBS). Virus plaque titrations were performed in 6-well plates of

confluent Vero or LLC-MK₂ cells as described previously (Miller et al., *Am. J. Trop. Med. & Hyg.* 35: 1302-1309 (1986)). The first 4-ml overlay medium -- containing 1% SeaKem LE agarose (FMC BioProducts, Rockland, Maine) in nutrient medium (0.165% lactalbumin hydrolysate [Difco Laboratories, Detroit, Mich.]), 0.033% yeast extract [Difco], Earl's balanced salt solution, 25 mg/L of gentamycin sulfate [Bio Whittaker, Walkersville, Md.], 1.0 mg/L of amphotericin B [Fungizone, E. R. Squibb & Sons, Princeton, N.J.], and 2% FBS) -- was added after adsorption of the 200- μ l virus inoculum for 1.5 h at 37°C. Following incubation at 37°C for 7 days, a second 2-ml overlay containing an additional 80 μ g/ml of neutral red vital stain (GIBCO-BRL, Gaithersburg, Md.) was added. Plaques were counted 8 to 11 days after infection.

Construction of chimeric D2/1 infectious clones

pD2-16681-P48, pD2-PDK53-E48, pD2-PDK53-V48 vectors

Three DEN-2 vectors were used for construction of the chimeric D2/1 clones.

These were modified from the DEN-2 infectious clones reported by Kinney et al. (*Virology* 230: 300-308 (1997)). Clone pD2-16681-P48 was modified from pD2/IC-30P-A to contain cloning sites MluI and NgoMIV at nucleotide positions 451 and 2380, respectively. The same cloning sites were introduced into both DEN-2 PDK-53 virus-specific clones, pD2/IC-130Vx-4 and -130Vc-K, and the modified clones were designated as pD2-PDK53-E48 and pD2-PDK53-V48, respectively. Two cloning errors were found in the original pD2/IC-130Vx-4 and -130Vc-K at nt-6665 and nt-8840. These defects were corrected in pD2-PDK53-E48 and -V48. The introduced NgoMIV cloning site resulted in two nucleotide mutations (nt 2381 and 2382; TG to CC), which encoded a Val-to-Ala substitution at E-482. The nucleotide changes introduced at the MluI site were silent. The MluI site introduced at the C/prM junction was used to clone the prM-E genes of heterologous viruses.

Chimeric pD2/1-PP, -EP, -VP, -PV, -EV, and -VV

Two intermediate DEN-2 clones, pD2I-P and pD2I-E, were constructed by deleting the HpaI (nt-2676) to XbaI (3' terminus of viral genomic cDNA) fragments of pD2-16681-P48 and pD2-PDK53-E48, respectively. These intermediate clones were used to subclone DEN-1 virus-specific cDNA fragments. The cDNA fragments containing the C-prM-E genes of DEN-1 16007 or PDK-13 virus were amplified by reverse transcriptase - polymerase chain reaction (RT-PCR) from DEN-1 viral RNA with primers DEN-Bgl.5NC (5'-TAGAGAGCAGATCTCTG-3' (SEQ ID NO:31); conserved sequence in the 5'NCR of dengue viral genomes, underlined sequence is a BglII site) and cD1-2394.Ngo: (5'-TG TGACCATGCCGGCTGCGATGCACTCACCGA-3' (SEQ ID NO:32); underlined NgoMIV site followed by complementary sequence near the 3' end of the E gene of DEN-1 virus). Amplified fragments were cloned into the BglII-NgoMIV sites of the intermediate pD2I-P and pD2I-E clones. Intermediate, chimeric pD2/1 clones were sequenced to verify the accuracy of the inserted DEN-1 virus-specific cDNA. Fragments excised from the intermediate pD2/1 clones with SstI (preceding the T7 promoter) and NgoMIV were cloned into the full genome-length DEN-2 vectors, pD2-16681-P48, pD2-PDK53-E48, and pD2-PDK53-V48. Six full genome-length chimeric pD2/1 plasmids were constructed by inserting the C-prM-E gene region of DEN-1 16007 or PDK-13 virus into these three vectors (FIG. 1). The plasmids were designated pD2/1-XY and their virus derivatives were designated DEN2/1-XY, where X = the infectious DEN-2 clone background (P = parental 16881 clone, E = PDK53-E variant, V = PDK53-V variant) and Y = DEN-1 virus-specific C-prM-E insert (P = parental 16007 strain, V = PDK-13 vaccine candidate). The PDK53-E backbone contains three DEN-2 PDK-53 virus-specific amino acid mutations (NS1-53-Asp, NS2A-181-Phe and NS4A-75-Ala) as well as the 5'NC-57 mutation of PDK-53 virus. The PDK53-V backbone contains these same PDK-53 virus-specific loci plus the additional PDK-53 virus-specific NS3-250-Val locus.

Recovery of recombinant viruses

All recombinant plasmids were grown in *Escherichia coli* XL1-Blue cells. Recombinant viral RNA was transcribed and capped with the cap analog m⁷GpppA from 200-400 ng of XbaI-linearized cDNA, and transfected into 3-4 x 10⁶ LLC-MK₂ or BHK-21 cells by electroporation. Transfected cells were transferred to 75-cm² flasks in DMEM medium containing 10% FBS. Viral proteins expressed in the transfected cells were analyzed by indirect immunofluorescence assay (IFA). Virus-infected cells were fixed in ice-cold acetone for 30 min. DEN-1 and DEN-2 virus-specific monoclonal antibodies 1F1 and 3H5, respectively, were used in the assay, and binding was detected with fluorescein-labeled goat anti-mouse antibody. Viruses were harvested after 8 to 10 days, and were then passaged in LLC-MK₂ cells once (DEN-2-16681-P48, DEN-2-PDK53-E48 and -V48, DEN-2/1-PP, -EP, and -VP) or twice (DEN-2/1-PV, -EV, and -VV) to obtain working seeds. D2/1-EV and -VV viruses were passaged a third time in LLC-MK₂ cells to obtain higher viral titers required for challenge or immunization of mice.

Characterization of the replication phenotypes of chimeric viruses in cell cultures

Plaque sizes were measured 10 days after infection in LLC-MK₂ cells. Mean plaque diameters were calculated from 10 plaques for each virus. Viral growth curves were performed in 75-cm² flasks of LLC-MK₂ or C6/36 cells at approximately 0.001 multiplicity of infection (m.o.i.). After adsorption for 2 h, 30 ml of DMEM medium (for LLC-MK₂ cells) or overlay nutrient medium (for C6/36 cells) containing 5% FBS and penicillin/streptomycin was added, and the cultures were incubated in 5% CO₂ at 37°C or 29°C, respectively. Aliquots of culture medium were harvested at 48-h intervals for 12 days, adjusted to 12.5% FBS, and stored at -80°C prior to titration.

Temperature sensitivity was tested in LLC-MK₂ cells. Cells grown in two sets of 75-cm² flasks were infected and incubated as described for the growth curve study. One set of cultures was incubated for 8 days at 37°C, the other at 38.7°C. The ratio of virus titer at 38.7°C versus the titer at 37°C was calculated. Virus was designated as

temperature-sensitive if the virus titer at 38.7°C was reduced 60% or greater, relative its titer at 37°C.

Sequencing of viral cDNA

- 5 Viral RNA was extracted from virus seed or by using the QIAmp Viral RNA kit (Qiagen, Valencia, Calif.). DEN-1 virus-specific primers were based on the published data of the Singapore strain S275/90 (Fu et al., *Virology* 88: 953-958 (1992)). Five to 7 overlapping viral cDNA fragments were amplified by RT-PCR with the Titan One-Tube RT-PCR System (Roche Molecular Biochemicals, Indianapolis, Ind.). Both
- 10 strands of the cDNA amplicons were sequenced directly. For sequencing of the DEN-1 PDK-13 viral genome, template genomic RNA was extracted directly from a vial of the candidate DEN-1 PDK-13 vaccine (lot March 10, 1989). The 5'- and 3'- terminal sequences of the DEN-1 16007 and DEN-1 PDK-13 viral genomes were determined with the 5' RACE kit (GIBCO BRL) and by tailing the genomic RNA with poly(A).
- 15 Automated sequencing was performed as recommended on a PRISM 377 sequencer (Perkin-Elmer/Applied Biosystems, Foster City, Calif.).

Mouse studies

- Litters of newborn, 1-day-old outbred white ICR mice were inoculated
- 20 intracranially with 5,000 PFU of virus in a volume of 30 µl. They were observed daily for paralysis and death, and surviving mice were individually weighed once each week for 5 weeks.

- Neutralizing antibody responses were tested in 3-week-old ICR mice. They
- 25 were inoculated intraperitoneally with 10⁴ PFU of virus, and were boosted with the same amount of virus 3 weeks or 6 weeks later. Mice were bled 2 days prior to the boost and 3 weeks after boosting.

The ICR strain of inbred mice used above are not usually fatally susceptible to challenge with wild-type DEN-1 virus. Therefore, to fully test the ability of the DEN-2/1 viral chimera to induce an effective immune response, it was necessary to utilize inbred AG-129 mice, which lack receptors for both interferon alpha/beta and interferon gamma (Muller et al., *Science* 264:1918-1921 (1994)), as these mice have been found to be susceptible to intraperitoneal challenge with high doses of wild-type DEN-1 virus, strain Mochizuki. Therefore, 3.5-4.5-week-old inbred AG-129 mice were immunized intraperitoneally with 10^4 PFU of wild-type DEN-1 16007, Mahidol candidate vaccine DEN-1 PDK-13, chimeric DEN-2/1-EP or chimeric DEN-2/1-VP virus. These immunized mice were challenged intraperitoneally with a lethal dose of DEN-1 Mochizuki virus.

Neutralization Assays

Mouse serum samples were tested for neutralizing antibodies by serum- dilution plaque-reduction neutralization test (PRNT). Sixty PFU of DEN-1 16007 virus was incubated with serial 2-fold dilutions of heat-inactivated (56°C for 30 min) mouse serum specimens overnight at 4°C. The neutralizing antibody titer was identified as the highest serum dilution that reduced the number of virus plaques in the test by 50% or greater.

Results

To assess the potential of infectious cDNA clones derived from the two variants of DEN-2 16681 PDK-53 virus (PDK-53-E and PDK-53-V) to serve as vectors for vaccine development, we engineered chimeric DEN-2/DEN-1 cDNA clones (D2/1-EP, D2/1-VP, D2/1-EV, and D2/1-VV) containing the structural genes (C-prM-E) of wild-type DEN-1 16007 virus or its vaccine derivative, strain PDK-13, within the backbone of these two vectors (FIG. 1). Two other chimeric clones, D2/1-PP and D2/1-PV, containing the structural genes (C-prM-E) of DEN-1 16007 or PDK-13 virus in the backbone of wild-type DEN-2 16681 virus, were also constructed for comparison (FIG. 1). We sequenced the entire full-length genomic cDNA in all of the infectious clones.

A silent cDNA artifact was incorporated into the chimeric clones at nt-297 (T-to-C). A silent mutation at nt-1575 (T-to-C) was engineered into all of the chimeric clones to remove the natural XbaI site in the E gene of the DEN-1 virus.

5 Titers after transfection of LLC-MK₂ or BHK-21 cells were 10^4 - 10^6 PFU/ml for the chimeric viruses D2/1-PP, -EP, and -VP containing the C-prM-E of DEN-1 16007 virus. These titers increased to $10^{6.5}$ - $10^{7.5}$ PFU/ml after a single passage in LLC-MK₂ cells, comparable to the titers obtained for their parental viruses. Lower titers of 10^2 - 10^4 PFU/ml were obtained in transfected cells for the chimeric DEN-2/1-PV, -EV, and -
10 VV viruses containing the C-prM-E of DEN-1 PDK-13 virus. D2/1-PV virus reached 10^6 PFU/ml after 2 passages in LLC-MK₂ cells, whereas D2/1-EV and -VV viruses reached titers of $10^{3.3}$ - $10^{5.3}$ PFU/ml after two or three passages. Cells infected with any of the chimeric DEN-2/1 viruses were positive by IFA with monoclonal antibody 1F1 (specific for DEN-1 E protein) and negative with monoclonal antibody 3H5
15 (specific for DEN-2 E protein), indicating that appropriate DEN-1 E proteins were expressed by the chimeras. The DEN-2/1-PP, DEN-2/1-EP, and DEN-2/1-VP viral genomes were fully sequenced by directly analyzing overlapping RT-PCR fragments amplified from genomic viral RNA extracted from master seeds. All three genomes had the expected sequence.

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Growth of the chimeric viruses in LLC-MK₂ and C6/36 cell cultures

All of the chimeric DEN-2/1 viruses produced smaller plaques, relative to the 6.8 ± 0.4 -mm plaque of wild-type DEN-1 16007 virus in LLC-MK₂ cells (FIG. 2A). Both DEN-2/1-EP (3.1 ± 0.3 mm) and -VP (2.8 ± 0.3 mm) viral plaques were similar in
25 size to those of DEN-1 PDK-13 virus (2.9 ± 0.3 mm). The chimeric viruses DEN-2/1-PV, DEN-2/1-EV, and DEN-2/1-VV containing the C-prM-E of DEN-1 PDK-13 virus formed tiny (1.3 ± 0.3 mm) or pinpoint (<1 mm) plaques. The DEN-2 16681-P48 virus produced 3.5 ± 0.3 -mm plaques that were similar to plaques of wild-type DEN-2 16681 virus. The DEN-2 PDK53-V48 virus formed plaques that were smaller and fuzzier
30 than those of the DEN-2 PDK53-E48 virus. The 5.1 ± 0.3 -mm plaques of DEN-2/1-PP

virus were larger than those of the other chimeric viruses, but smaller than those of DEN-1 16007 virus.

Viruses were tested for temperature sensitivity in LLC-MK₂ cells. Temperature sensitivity was determined on day 8 or 10 after infection as indicated in FIG. 2B. Temperature sensitivity was based on the reduction of virus titers at 38.7°C from those at 37°C. Temperature sensitivity was calculated from measurements taken in at least 3 experiments.

The DEN-2 PDK53-V variant (D2-PDK53-V48) was more temperature sensitive than DEN-2 PDK53-E virus (D2-PDK53-E48) and DEN-2 16681 virus (DEN-2-16681-P48) was somewhat temperature sensitive (70-87% titer reduction at 38.7°C). Multiple temperature sensitivity tests for DEN-2-PDK53-E48 virus resulted in 83%-97% growth reduction. The titer of DEN-1 16007 virus was reduced by 40% or less at 38.7°C, making it the least-temperature sensitive virus in this study. All of the chimeric viruses were temperature sensitive relative to DEN-1 16007 virus, and were at least as temperature-sensitive as PDK-13.

All of the DEN-1, DEN-2, and chimeric D2/1 viruses reached peak titers between 8 and 10 days after infection in LLC-MK₂ cells (FIG. 2B). The clone-derived viruses DEN-2-16681-P48, DEN-2-PDK53-E48, and DEN-2-PDK53-V48 replicated to 10^{7.0} PFU/ml or greater, as did DEN-2 16681 and PDK-53 viruses. Although reaching similar peak titer, DEN-2-PDK53-V48 virus replicated slower than the DEN-2-PDK53-E48 virus during the first 4 days after infection. Chimeric DEN-2/1-PP, DEN-2/1-EP, DEN-2/1-VP, and DEN-2/1-PV viruses reached peak titers over 10^{6.7} PFU/ml, comparable to the peak titers of their parental DEN-1 and DEN-2 viruses. Chimeric DEN-2/1-EV and -VV viruses, which had peak titers of 10^{5.6}-10^{5.9} PFU/ml or lower in several separate experiments, replicated less efficiently than the other viruses.

The PDK-13 virus-specific chimeras result in lower virus titers recovered from transfected cells, relative to the 16007 virus-specific chimeras. Previous experiences with DEN-2/DEN-1 and DEN-2/DEN-4 chimeras indicate that chimeric viruses which exhibit crippled replication during transfection and later develop high virus titers after
5 passage in cell culture often accrued unexpected mutations. Viruses of increased replicative ability may arise through selection of subpopulations of virus variants, resulting from incorporation errors during *in vitro* transcription of cDNA. Chimeric viruses that replicate well in transfected cells were more genetically stable after passage in LLC-MK₂ cells. Efficient replication with minimal passage in mammalian cell
10 culture may be an important criterion of genetic stability and suitability for an infectious clone-derived vaccine virus.

Viral growth curves in C6/36 cells were monitored following infection of C6/36 cells at an approximate multiplicity of 0.001 PFU/ml (FIG. 3). The three DEN-2
15 backbone viruses, DEN-2-16681-P48, DEN-2-PDK53-E48 and DEN-2-PDK53-V48, replicated like the original DEN-2 16681 virus and the two PDK-53 variants, respectively. Both DEN-2-PDK53-E48 and DEN-2-PDK53-V48 viruses replicated about 4000-fold less efficiently than the DEN-2-16681-P48, DEN-1 16007 and PDK-13 viruses in C6/36 cells. DEN-1 16007 and PDK-13 viruses replicated to high titers
20 of $10^{8.7}$ and $10^{8.4}$ PFU/ml, respectively. The chimeric DEN-2/1-PP virus replicated to $10^{5.2}$ PFU/ml, which was equivalent to the peak titers of the two DEN-2-PDK53 variants. Replication of chimeric DEN-2/1-EP and DEN-2/1-VP viruses was very inefficient in C6/36 cells. These viruses reached peak titers of lower than 10^2 PFU/ml.

25 Neurovirulence in suckling mice

Groups of newborn to one-day-old ICR mice (n=16) were inoculated intracranially with 5000 PFU of virus. Wild-type DEN-2 16681 virus was 100% fatal with average survival time at 14.1 ± 1.6 days, while both clone-derived DEN-2-PDK53-E48 and DEN-2-PDK53-V48 viruses failed to kill any ICR mice. Unlike DEN-
30 2 16681 virus, which typically kills 50% or greater of challenged mice, the wild-type

DEN-1 16007 virus caused only a single fatality (21 days after challenge) in the ICR mice. The DEN-1 PDK-13 virus did not kill any of the ICR mice. DEN-1 16007 virus-infected ICR mice had significantly lower mean body weights ($p < 0.00003$, Student's t test), relative to the control group inoculated with diluent, between 21-35 days after challenge. All of the ICR mouse groups challenged with five chimeric DEN-2/1 viruses (DEN-2/1-VV virus was not tested) had lower mean weights ($p < 0.02$) when compared to the control group, but their mean weights were significantly greater ($p < 0.004$) than the DEN-1 16007 group 28 days after infection. The mean body weights of ICR mouse groups challenged with 10^4 PFU of DEN-1 16007 or PDK-13 virus were nearly identical to those of the ICR mice challenged with 5000 PFU of DEN-1 16007 virus between 7-35 days after challenge.

Immunogenicity of chimeric DEN-2/1 viruses in mice

Outbred ICR Mice: To test the immunogenicity of the chimeric viruses, groups of 3-week-old ICR mice ($n=8$) were immunized intraperitoneally with 10^4 PFU of virus in Experiment 1 and Experiment 2 (Table 7). In Experiment 1, the mice were bled 20 days after primary immunization and then boosted 2 days later. In Experiment 2, the mice were bled 41 days after primary immunization and boosted 2 days later. Table 7 shows the reciprocal, 50% plaque-reduction endpoint PRNT titers of the pooled serum samples from each immunized group. The range of individual titers for the eight mice in many of the groups is also shown. In both experiments, the reciprocal titer of the pooled serum from 16007 virus-immunized mice was 80 before boost and 2560 after boost. In both experiments, mice immunized with chimeric DEN-2/1-PP, -EP, or DEN-2/1-VP viruses had a pooled serum titer that was at least as high as those of the 16007 virus-immunized groups before (reciprocal titers of 40-160) and after (reciprocal titers of 2560-5210) boost. The immune responses of the mice in these virus groups were nearly equivalent in both Experiment 1 and Experiment 2.

The PDK-13 virus and all three of the chimeras containing the PDK-13 structural genes induced minimal or low reciprocal PRNT titers of 10-20 against DEN-

1 16007 virus by 20 days after primary immunization in Experiment 1. A somewhat
higher reciprocal PRNT titer of 40 was elicited by each of these viruses by 41 days
after immunization in Experiment 2. The development of neutralizing antibodies was
slower and of lower magnitude following immunization with PDK-13, DEN-2/1-PV, -
5 EV, or -VV virus than with 16007, DEN-2/1-PP, -EP, or -VP virus in these mice. One
mouse in the DEN-2/1-PV group in Experiment 1 and one mouse in each of the DEN-
2/1-EV groups in both experiments failed to produce a detectable PRNT titer before
boost. Boosted titers were also higher for the PDK-13, DEN-2/1-PV, -EV, and -VV-
immunized groups in Experiment 2 (pooled reciprocal titers of 160-2560) than in
10 Experiment 1 (pooled reciprocal titers of 80). Except for the DEN-2/1-PV group in
Experiment 2, these boosted titers were lower than the boosted PRNT titers induced by
wild-type 16007 virus and chimeric DEN-2/1-PP, -EP, and -VP viruses containing the
structural genes of the wild-type DEN-1 16007 virus (Table 7). The high PRNT titer
obtained for the pooled serum of the mice boosted with DEN-2/1-PV virus resulted
15 from two mouse sera which had reciprocal titers of 2560 and 10,240. The remaining 6
mice in this group had reciprocal titers of 20 to 640, which were similar to the
individual titers of mice in the PDK-13, DEN-2/1-EV, and -VV groups. The PDK-13,
DEN-2/1-PV, DEN-2/1-EV, and DEN-2/1-VV viruses appeared to be less
immunogenic than the 16007, DEN-2/1-PP, -EP, and -VP viruses in these outbred
20 mice. Pooled serum samples from mice immunized with DEN-2-16681-P48, DEN-2-
PDK-53-E48, or DEN-2-PDK-53-V48 virus did not contain detectable cross
neutralizing antibody against DEN-1 16007 virus.

Inbred AG-129 Mice: To test the immunogenicity of the chimeric viruses,
25 groups of 3.5-4.5-week-old inbred AG-129 mice were immunized intraperitoneally
with 10^4 PFU of wild-type DEN-1 16007, Mahidol candidate vaccine DEN-1 PDK-13,
chimeric DEN-2/1-EP, or chimeric DEN-2/1-VP virus. At 26 days after primary
immunization, pooled sera from mice immunized with chimeric DEN-2/1-EP or DEN-
2/1-VP virus had reciprocal 70% serum dilution-plaque reduction neutralizing
30 antibody titers (PRNT_{70}) of 80-160. These titers were equivalent (within 2-fold) of the

neutralizing antibody response elicited by the candidate DEN-1 PDK-13 vaccine, but lower than the 640 titer elicited by the wild-type DEN-1 16007 virus. Control mice injected intraperitoneally with phosphate buffered saline had titers of less than 10. All mice were challenged intraperitoneally with 10^7 PFU of wild-type, virulent DEN-1 virus, strain Mochizuki, at 28 days after primary immunization. All eleven of the control, non-immunized mice died within 21 days (average survival time of 11.5 ± 4.2 days [mean \pm standard deviation]) after challenge, whereas all of the DEN-1 (16007, PDK-13, DEN-2/1-EP, DEN-2/1-VP) virus-immunized mice survived challenge with DEN-1 Mochizuki virus. At 34 days after challenge with DEN-1 Mochizuki, all of the virus-immunized mice had reciprocal PRNT₇₀ titers of 1280-2560. The chimeric DEN-2/1-EP and DEN-2/1-VP viruses were highly immunogenic and protective for AG-129 mice.

Nucleotide sequence analyses of DEN-1 16007 and PDK-13 viral genomes

We sequenced the genomes of wild-type DEN-1 16007 virus (GenBank accession number AF180817) and its PDK-13 vaccine derivative (accession number AF180818). There were 14 nucleotide and 8 encoded amino acid differences between 16007 and PDK-13 viruses (Table 2). Silent mutations occurred at genome nucleotide positions 1567, 2695, 2782, 7330, and 9445 in the E, NS1, NS4B, and NS5 genes. Unlike the candidate DEN-2 PDK-53 vaccine virus, which has no amino acid mutations in the E protein, the DEN-1 PDK-13 virus had five amino acid mutations in E, including E-130 Val-to-Ala, E-203 Glu-to-Lys, E-204 Arg-to-Lys, E-225 Ser-to-Leu, and E-447 Met-to-Val. Amino acid mutations in the nonstructural genes included NS3-182 Glu-to-Lys, NS3-510 Tyr-to-Phe, and NS4A-144 Met-to-Val. The PDK-13 virus-specific E-477-Val was incorporated into all of the chimeric constructs.

Immunization of monkeys with chimeric DEN-2/1 viruses

The immunogenicity of the chimeric DEN-2/1-EP and DEN-2/1-VP viruses in adult crab-eating monkeys (*Macaca fascicularis*) was tested. Immunization of monkeys was accomplished by means of subcutaneous injection with 10^6 PFU of

chimeric DEN-2/1-EP or DEN-2/1-VP virus. Sera obtained from the immunized monkeys were analyzed for the presence of viremia by direct plaque assay of serum aliquots in LLC-MK₂ cell monolayers maintained under agarose overlay in 6-well plates, and by inoculation of serum aliquots into cultures of LLC-MK₂ cells maintained in liquid medium. No infectious virus was identified in any of the monkey sera by either of these two classical assay methods. By these two virus assays, no viremia was detectable following immunization with either chimeric DEN-2/1-EP or DEN-2/1-VP virus. Monkey sera were tested for DEN-1 virus-specific neutralizing antibodies. At 30 days after primary immunization, sera from three individual monkeys immunized with chimeric DEN-2/1-EP virus had reciprocal 50% serum dilution-plaque reduction neutralizing antibody titers (PRNT₅₀) of 80, 160 and 1280. Sera from three individual monkeys immunized with chimeric DEN-2/1-VP had reciprocal PRNT₅₀ titers of 160, 160 and 640. Monkeys injected with diluent as a control for the experiment had reciprocal PRNT₅₀ titers of less than 10, as did all of the monkeys just prior to immunization. The chimeric DEN-2/1-EP and -VP viruses elicited DEN-1 virus-specific neutralizing antibodies in non-human primates.

Example 2

Construction Of Chimeric DEN-2/3 Infectious Clones

An in vitro ligation strategy was used for the full genome-length DEN-2/3 infectious clones.

(i) 5'-end DEN-2/3 intermediate clones: pD2I/D3-P1-Asc and pD2I/D3-E1-Asc

Intermediate DEN-2 clones, pD2I-P and pD2I-E were used to subclone the DEN-3 16562 virus-specific cDNA fragment. The cDNA fragment containing the prM-E genes of wild-type DEN-3 16562 virus was amplified by reverse transcriptase - polymerase chain reaction (RT-PCR) from DEN-3 viral RNA with primers D3-435.Mlu:

(5'-TGCTGGCCACTTAACTACGCGTGATGGAGAGCCGCGCA-3' (SEQ ID NO:33); underlined MluI site followed by DEN-3 virus sequence near the 5' end of the

prM gene) and cD3-2394.Ngo:
 (5'-TGTAATGATGCCGGCCGCGATGCATGAAAATGA-3' (SEQ ID NO:34);
 underlined NgoMIV site followed by complementary sequence near the 3' end of the E
 gene of DEN-3 virus). The MluI site contained a silent mutation for DEN-2 virus at
 5 amino acid prM-5-Thr. This position is Ser in DEN-3 virus, but Thr in chimeric DEN-
 2/3 virus. The NgoMIV site resulted in a Val-to-Ala substitution at E-482 of DEN-2
 virus, and an Ile-to-Ala substitution at E-480 of DEN-3 virus. The amplified fragment
 was cloned into the MluI-NgoMIV sites of the intermediate pD2I-P and pD2I-E clones.
 A restriction site, AscI, was introduced downstream of the NgoMIV site by site-
 10 directed mutagenesis to facilitate *in vitro* ligation. This unique AscI site was only 16 nts
 downstream from the NgoMIV site and was excised prior to *in vitro* ligation of the full-
 length DEN-2/3 clones. An additional mutagenesis at nt 1970 (A-to-T) which changed
 amino acid E-345 from His to Leu, was introduced to permit derivation of viable
 chimeric viruses in LLC-MK₂ cells, as explained below. These intermediate chimeric
 15 DEN-2/3 clones, pD2I/D3-P-Asc and pD2I/D3-E-Asc, were sequenced to verify the
 accuracy of the inserted DEN-3 virus-specific cDNA. A silent mutation was
 incorporated at nt 552 (C-to-T) in both intermediate chimeric clones.

(ii) 3'-end DEN-2 intermediate clones: pD2-Pm^ab-Asc, pD2-Em^ab-Asc, and pD2-
 20 Vm^ab-Asc

Intermediate DEN-2 clones containing the truncated DEN-2 virus-specific
 cDNA sequence from nt 2203-10723 (3'-end) of DEN-2 16681, PDK53-E, or PDK-53-
 V virus were obtained by deletion of the 5'end (including T7 promoter sequence and
 DEN-2 nts 1-2202) of the virus specific cDNA in the full-length clones, pD2-16681-
 25 P48, pD2-PDK53-E48, and pD2-PDK53-V48, respectively. An AscI site was also
 introduced at nt 2358 (22 nts upstream of the NgoMIV site) to facilitate the *in vitro*
 ligation. This AscI site was excised prior to performing the *in vitro* ligation of the full
 genome-length, chimeric DEN-2/3 infectious clones.

(iii) Full-length chimeric DEN-2/3 cDNA: DEN-2/3-PP1, DEN-2/3-EP1, and DEN-2/3-VP1

Three to ten mg of the 5'-end pD2I/D3 and 3'-end D2 intermediate clones were digested by AscI, treated with calf intestine phosphatase (CIP), and then digested with
 5 NgoMIV. The excised small AscI-NgoMIV fragments were removed by passing the digested DNA through Qiagen PCR-purification spin columns. The large 5'- and 3'-end, linearized intermediate clones were then ligated together (5' : 3' = 1:3 molar ratio) to obtain full genome-length DEN-2/3-PP1 (pD2I/D3-P1-Asc ligated with pD2- Pm⁺b-Asc), DEN-2/3-EP1 (pD2I/D3-E1-Asc ligated with pD2-Em⁺b-Asc), and DEN-2/3-
 10 VP1 (pD2I/D3- E1-Asc ligated with pD2-Vm⁺b-Asc). These ligated DNAs were then cut with XbaI to produce the linearized 3'-end of the viral cDNA required for transcription of the recombinant viral RNA.

Recovery of chimeric DEN-2/3 viruses

15 Recombinant viral RNA was transcribed from XbaI- linearized cDNA and capped with the cap analog m⁷GpppA. LLC-MK₂ or BHK-21 cells (3- 5 x 10⁶ cells) were transfected by electroporation as described by Kinney et al. (*J. Virol* 230: 300-308 (1997)). Transfected cells were transferred to 75-cm² flasks in DMEM medium containing 10% FBS. Viral proteins expressed in the transfected cells were analyzed
 20 by indirect immunofluorescence assay (IFA). Virus-infected cells were fixed in ice-cold acetone for 30 min. DEN-3 and DEN-2 virus-specific monoclonal antibodies 8A1 and 3H5, respectively, were used in the assay, and binding was detected with fluorescein-labeled goat anti-mouse antibody. Viruses were harvested after 5 to 11 days, and were then passaged in LLC-MK₂ cells once to obtain working seeds. Viral
 25 genomes extracted from these seeds were sequenced to confirm the genotypes of the progeny viruses. An earlier strategy using 5'-end D2I/D3 intermediate clones containing authentic DEN-3 16562 prM-E genes resulted in mutations at several different positions in the genomes of the viruses recovered from transfected LLC-MK₂ or BHK-21 cells and passaged once in LLC- MK₂ cells. A mutation at nt 1970 from A
 30 to T, which changed amino acid E-345 from His to Leu, was found in seven of nine

independently recovered recombinant viruses. It was obvious that the original DEN-2/3 chimeric viruses were unstable in LLC-MK₂ and/or BHK-21 cells. The single mutation at E-345 was the only mutation that occurred in the genomes of three recovered viruses, indicating that this mutation might help to stabilize the viruses in culture. We
5 introduced this mutation in all the infectious DEN-2/3 clones and recombinant viruses recovered from such mutagenized clones proved to be stable in cell culture.

Example 3

Construction Of Chimeric DEN-2/4 Infectious Clones

10

pD2-16681-P48, pD2-PDK53-E48, pD2-PDK53-V48 vectors

The three DEN-2 backbone vectors used for construction of the chimeric DEN-2/4 clones were modified as described above. The DEN-2 infectious clones have been previously reported in Kinney et al., 1997. Clone pD2-16681-P48 was modified from
15 pD2/IC-30P-A to contain cloning sites MluI and NgoMIV at nucleotide positions 451 and 2380, respectively. The same cloning sites were introduced into both DEN-2 PDK-53 virus-specific clones, pD2/IC-130Vx-4 and -130Vc-K, and the modified clones were designated as pD2-PDK53-E48 and pD2-PDK53-V48, respectively. Two cloning errors were found in the original pD2/IC-130Vx-4 and -130Vc-K at nt-6665 and nt-
20 8840. These defects were corrected in pD2-PDK53-E48 and -V48. The introduced NgoMIV cloning site resulted in two nucleotide mutations (nt 2381 and 2382; TG to CC), which encoded a Val-to-Ala substitution at E-482 of DEN-2 virus. The nucleotide changes introduced at the MluI site were silent for DEN-2 virus and chimeric DEN-2/4 viruses. The MluI site (near the C/prM junction) and NgoMIV site
25 (close to E/NS1 junction) were used to clone the prM-E genes of heterologous viruses.

Chimeric pDEN-2/4-PP1, -EP1, and -VP1

Two intermediate DEN-2 clones, pD2I-P and pD2I-E, were constructed by deleting the HpaI (nt-2676) to XbaI (3' terminus of viral genomic cDNA) fragments of
30 pD2-16681-P48 and pD2-PDK53-E48, respectively. These intermediate clones were

used to subclone DEN-4 1036 virus-specific cDNA fragments. The cDNA fragment containing the prM-E genes of DEN-4 1036 virus was amplified by reverse transcriptase - polymerase chain reaction (RT-PCR) from DEN-4 viral RNA with primers D4-453Mlu:

5 (5'-GGCGTTTCACTTGTCAACGCGTGATGGCGAACCCCTCA-3' (SEQ ID NO:35); underlined MluI site followed by sequence near the 5' end of the DEN-4 1036 viral genome) and cD4-2394.Ngo:

(5'-AGTGATTCCGCCGGCAGCTATGCACGTCATAGCCAT-3' (SEQ ID NO:36); underlined NgoMIV site followed by complementary sequence near the 3' end of the E gene of DEN-4 virus). Amplified fragments were cloned into the MluI-NgoMIV sites of the intermediate pD2I-P and pD2I-E clones. Intermediate, chimeric DEN-2/4 clones were sequenced to verify the accuracy of the inserted DEN-4 virus-specific cDNA. A silent mutation was incorporated at nt 1401 (A-to-G) in both intermediate clones. Fragments excised from the DEN-2/IC-P48, -VE48, and -VV48 clones with NgoMIV and ScaI (downstream of DEN-2 cDNA sequence in these plasmids) were cloned into 15 NgoMIV/ScaI-cut chimeric D2/4 intermediate clones to obtain the full-length chimeric D2/4-PP, -EP, and -VP clones. However, transcribed RNA from these chimeric clones only produced viable DEN-2/4 chimeric viruses in transfected C6/36 cells, but not in transfected LLC-MK₂ cells. After passaging the chimeric viruses in C6/36 cells one 20 more time to obtain higher titers, these viruses were passaged in LLC-MK₂ cells five times to obtain stable chimeric DEN-2/4 viruses which replicated efficiently in LLC-MK₂ cells. Titers of the virus seeds increased from 200 PFU/ml at the first LLC-MK₂ cell passage to over 10⁶ PFU/ml at the fifth LLC-MK₂ cell passage.

25 The genomes of viruses from the first, second, third and fifth LLC-MK₂ cell passages of the chimeric DEN-2/4-PP viruses were sequenced. Four mutations, DEN-2 virus-specific, C-100 (Arg-to-Ser), DEN-4 virus-specific E-364 (Ala- to-Ala/Val mix), DEN-4 virus-specific E-447 (Met-to-Leu) and DEN-2 virus-specific NS4B-239 (Ile-to-Leu) were identified (amino acid positions based on chimeric DEN-2/4 virus 30 sequences). The three mutations located in the structural genes (C and E) were

introduced into the chimeric DEN-2/4-PP, -EP, and -VP infectious cDNA clones to obtain DEN-2/4-PP1, -EP1, and -VP1 clones, respectively. All three of these chimeric DEN-2/4 clones produced viable, high-titered chimeric viruses in LLC-MK₂ cells immediately after transfection indicating that these three mutations helped the viruses to replicate in LLC-MK₂ cells. Chimeric DEN-2/4 clones were also mutagenized to contain different combinations of the four mutations to determine which mutations are needed for replication efficiency of the chimeric DEN-2/4 viruses in LLC-MK₂ cells. The DEN-4 E-447 (Met-to-Leu) mutation alone or together with the DEN-4 E-364 mutation, in combination with the DEN-2 C-100 (Arg-to-Ser) mutation was adequate to allow derivation of DEN-2/4 virus in LLC-MK₂ cells.

Recovery of recombinant viruses.

Recombinant plasmids pD2/4-PP1, -EP1, and -VP1 all were grown in *Escherichia coli* XL1-Blue cells. Recombinant viral RNA was transcribed and capped with the cap analog m⁷GpppA from 200-400 ng of XbaI-linearized cDNA, and transfected into 3-5.10⁶ LLC-MK₂ cells. Transfected cells were transferred to 75-cm² flasks in DMEM medium containing 10% FBS. Viral proteins expressed in the transfected cells were analyzed by indirect immunofluorescence assay (IFA). Virus-infected cells were fixed in ice-cold acetone for 30 min. DEN-4 and DEN-2 virus-specific monoclonal antibodies 1H10 and 3H5, respectively, were used in the assay, and binding was detected with fluorescein-labeled goat anti-mouse antibody. Viruses were harvested after 8 to 10 days, and were then passaged in LLC-MK₂ cells once to obtain working seeds. The genomes of all these three working seeds were fully sequenced, and all the chimeric DEN-2/4 viral genomes contained the expected sequences. The nucleotide and amino acid sequences for the DEN 2/4 chimera are provided herein at SEQ ID NO:13 and SEQ ID NO:14, respectively.

Example 4***Characterization of DEN-2/3 and DEN-2/4 Chimeric Viruses***

The viable, infectious chimeric DEN-2/3 and DEN-2/4 viruses, which express
5 the prM/E gene region of wild-type DEN-3 16562 or wild-type DEN-4 1036 virus,
respectively, expressed appropriate DEN-3 or DEN-4 virus-specific envelope protein
(E) epitopes, as analyzed by indirect immunofluorescence of virus-infected LLC-MK₂
cells with virus-specific anti-E monoclonal antibodies. These chimeric viruses, as well
as chimeric DEN-2/1 virus, also expressed appropriate DEN serotype-specific
10 neutralization epitopes when tested against standard polyvalent mouse ascitic fluids or
monoclonal antibodies in serum dilution-plaque reduction neutralization tests (Table 8).
The chimeric DEN-2/1-EP, DEN-2/3-EP1, and DEN-2/4-EP1 viruses were neutralized
by these standard DEN virus-specific antibodies to reciprocal PRNT₅₀ titers that were at
least as high as those that occurred for wild-type DEN-1, DEN-3, and DEN-4 viruses,
15 respectively (Table 8). These neutralization data indicated that the chimeric DEN-2/1,
DEN-2/3, and DEN-2/4 viruses expressed appropriate DEN serotype-specific
neutralization epitopes of DEN-1, DEN-3, and DEN-4 viruses, respectively.

20 Replication in LLC-MK2 cells

The replication and temperature sensitivity of DEN-2/3 chimeras in LLC-MK2
cells was monitored as the replication and temperature sensitivity of DEN-2/1 chimeras
was examined in Example 1. The chimeric DEN-2/3-PP1, -EP1, and -VP1 viruses and
chimeric DEN-2/4-PP1, -EP1, and -VP1 viruses, which expressed the prM/E gene
25 region of DEN-3 16562 virus or DEN-4 1036 virus in the genetic background of DEN-
2 16681 (-PP1), DEN-2 PDK-53-E variant (-EP1), or the DEN-2 PDK-53-V variant (-
VP1), respectively, all replicated to high peak titers of at least 10^{6.3} PFU/ml in LLC-
MK₂ cells. As defined in terms of the reduction of virus titers at 38.7°C versus those at
37°C (-, +, 2+, 3+ indicate titer reduction of less than or equal to 60%, 61-90%, 91-
30 99%, >99%, respectively, calculated from at least 3 experiments). Chimeric DEN-2/3-

PP1 and DEN-2/4-PP1 viruses exhibited either borderline temperature sensitivity (DEN-2/3-PP1) or no temperature sensitivity (DEN-2/4-PP1). The chimeric DEN-2/3-EP1 and -VP1, as well as the chimeric DEN-2/4-EP1 and -VP1 viruses, all of which were constructed in the genetic background of the DEN-2 PD-53-E or -V variant, retained the temperature-sensitive phenotypes that were exhibited by the two PDK-53 variant viruses (DEN-2-PDK53-E48 and -V48 viruses, respectively). The chimeras constructed in the background of the PDK-53-V variant exhibited a higher degree of temperature sensitivity than did those constructed in the background of the PDK-53-E variant.

10

Plaque sizes in LLC-MK2 cells

The plaque size resulting from inoculation of LLC-MK2 cells placed under agarose overlay, used as a biological marker to determine attenuation as described in Example 1, was also examined for the chimeric DEN-2/3 and DEN-2/4 viruses.

15 Average plaque size in mm follows each virus or chimera in brackets: DEN-3-16562 (6.6), DEN-2/3-PP1 (5.4), DEN-2/3-EP1 (4.5), DEN-2/3-VP1 (2.3), DEN-4-1036 (8.6), DEN-2/4-PP1 (3), DEN-2/4-EP1 (1.5), DEN-2/4-VP1 (1.2), DEN-2-16681-P48 (4.2), DEN-2-PDK53-E48 (2.5) and DEN-2-PDK-53-V48 (1.8).

20 The plaque sizes of the DEN-2/3-PP1 and DEN-2/4-PP1 viruses exhibited mean plaque diameters that were larger than those of the DEN-2 16681 or PDK-53 virus (as described in Example 1), but smaller than those of wild-type DEN-3 16562 and DEN-4 1036 viruses, respectively. This indicates that structural genes from the donor DEN-3 and DEN-4 viruses and capsid and/or nonstructural gene regions in the recipient genetic background of DEN-2 16681 virus both affected plaque size. The chimeric DEN-2/3-EP1 and -VP1 and DEN-2/4-EP1 and -VP1 viruses exhibited significant reductions in plaque size, relative to wild-type DEN-3 16562 and DEN-4 1036 viruses, respectively. The DEN-2 PDK-53 background-specific effect on plaque size may result from synergistic interaction of the mutations at the NS1-53 and NS3-250 loci of DEN-2

25

30 PDK-53 virus. Consequently, -VP1 chimeras exhibited greater reductions in plaque

size than did the -EP1 chimeras. The chimeric DEN-2/1, DEN-2/3, and DEN-2/4 viruses constructed in the genetic background of the candidate DEN-2 PDK-53 vaccine virus retained the phenotype of decreased plaque size as exhibited by DEN-2 PDK-53 virus.

5

Replication in C6/36 cells

The ability of the viruses to replicate in mosquito C6/36 cell culture, used as a biological marker to determine attenuation as described in Example 1, was also examined for the chimeric DEN-2/3 and DEN-2/4 viruses. Average peak titers in units of Log₁₀ PFU/ml follow each virus or chimera in brackets; D3-16562 (7.3), DEN-2/3-PP1 (7.6), DEN-2/3-EP1 (5.2), DEN-2/3-VP1 (5.7), D4-1036 (8.7), DEN-2/4-PP1 (7.8), DEN-2/4-EP1 (4.5), DEN-2/4-VP1 (4.4), DEN-2-16681-P48 (8.3), DEN-2-PDK53-E48 (5.4) and DEN-2-PDK-53-V48 (5).

Both of the Mahidol candidate DEN-2 PDK-53 variants exhibit decreased replication efficiency, relative to wild-type DEN-2 16681 virus, in mosquito C6/36 cell culture (DEN-2-PDK-53-E48 and -V48 versus DEN-2-16681-P48 virus). The decreased replication ability in C6/36 cells has been attributed to the mutations at the two 5'-NC-57 and NS1-53 loci in the DEN-2 PDK-53 virus; consistent with this view, both variants replicated to equivalently reduced peak titers in these cells. This crippled replication phenotype in C6/36 cells was retained in the chimeric DEN-2/3-EP1 and -VP1 and DEN-2/4-EP1 and -VP1 viruses, all of which replicated to lower peak titers than did the wild-type DEN-3 16562 or DEN-4 1036 virus, respectively. The chimeric DEN-2/3-PP1 and DEN-2/4-PP1 viruses, constructed in the genetic background of wild-type DEN-2 16681 virus, replicated to essentially the same extent (DEN-2/3-PP1) as or somewhat lower (DEN-2/4-PP1) than the wild-type DEN-3 16562 and DEN-4 1036 viruses, respectively. These results indicate that the replication-crippling effect of the 5'-NC-57 and NS1-53 loci in the DEN-2 PDK-53 virus-specific background was preserved in those chimeric viruses that were constructed within the DEN-2 PDK-53 genetic background.

Neurovirulence for newborn mice

Newborn, outbred, white ICR mice (n=16 for each group) were challenged intracranially with 10^4 PFU of wild-type DEN-3 and DEN-4 viruses, Mahidol candidate vaccine DEN-3 and DEN-4 viruses, chimeric DEN-2/3-PP1, -EP1, -VP1 viruses, and
5 chimeric DEN-2/4-PP1, -EP1, and -VP1 viruses (Table 9). The wild-type DEN-3 16562 and DEN-4 1036 viruses, which reliably caused 100% fatality in newborn mice, constituted a more sensitive model for attenuation of viral neurovirulence than does the DEN-2 16681 challenge model, which results in 50-100% fatality in newborn mice challenged with this virus. Interestingly, the Mahidol candidate DEN-4 PDK-48
10 vaccine virus also resulted in 100% fatality in challenged mice, although the average survival time of these mice was about two days longer than for mice challenged intracranially with wild-type DEN-4 1036 virus (Table 9). Like the DEN-2 PDK-53 vaccine virus and both of its variant populations, the chimeric DEN-2/3-EP1 and -VP1 and chimeric DEN-2/4-EP1 and -VP1 viruses were attenuated (no fatalities) for
15 newborn mice. This attenuation may be attributable, at least in part, to the attenuated DEN-2 PDK-53 genetic background of these chimeric viruses, because the chimeric DEN-2/4-PP1 virus exhibited significant neurovirulence (62.5% mortality) in these mice. This latter chimera was constructed in the genetic background of wild-type DEN-2 16681 virus.

20

Immunization of AG-129 mice with chimeric DEN-2/3 and DEN-2/4 viruses

Inbred AG-129 mice were immunized intraperitoneally with 10^5 PFU of wild-type or Mahidol vaccine candidate DEN-3 or DEN-4 virus or with 10^5 PFU of chimeric DEN-2/3-EP1 or DEN-2/4-EP1 virus (Table 10). The chimeric DEN-2/3-EP1 virus
25 elicited reciprocal PRNT₇₀ titers of 80-320 at 4-6 weeks after primary immunization. These titers were essentially equivalent to those elicited by the Mahidol DEN-3 vaccine

virus (strain PGMK-30/FRhL-3). However, the chimeric DEN-2/4-EP1 virus elicited neutralizing antibody titer of 20-40, which was lower than the 80-320 titer elicited by the Mahidol vaccine candidate DEN-4 PDK-48 vaccine virus. Nevertheless, both chimeric DEN-2/3 and DEN-2/4 viruses elicited neutralizing antibody responses in
5 AG-129 mice.

Example 5

Attenuation of a Dengue-2 Vaccine Virus: Strain 16681 (PDK-53)

Viruses and cell cultures

10 The parental DEN-2 16681 virus, several intermediate PDK passages (PDK-5, -10, -14, -35, and -45) of 16681 virus, recombinant 16681/PDK-53 viruses, and the genetically characterized LLC-MK₂-1 passage of the candidate PDK-53 vaccine virus were investigated.

15 Cell cultures of BHK-21 (clone 15), LLC-MK₂, Vero, and C6/36 were grown in Dulbecco's modified minimal essential medium (DMEM) supplemented with 10% heat-inactivated (56°C for 30 min) fetal bovine serum (FBS; HyClone Laboratories, Inc., Logan, Utah), 3.7 g/L of sodium bicarbonate (GIBCO-BRL, Life Technologies, Gaithersburg, Md.), 100 units/ml of penicillin G, and 100 mg/ml of streptomycin
20 sulfate (GIBCO-BRL).

Plaque titrations were performed in confluent monolayers of Vero cells in plastic 6-well plates as described previously (Miller et al., *Am. J. Trop. Med. & Hyg.* 35: 1302-1309 (1986)). A 200- μ l inoculum of virus was adsorbed for 1.5 h at 37°C,
25 followed by the addition of 4 ml of agarose overlay medium containing 1% SeaKem LE agarose (FMC BioProducts, Rockland, Md.) in nutrient medium (0.165 % lactalbumin hydrolysate [Difco Laboratories, Detroit, Mich.], 0.033% yeast extract [Difco], Earl's balanced salt solution, 25 mg/L of gentamicin sulfate [Bio Whittaker, Walkersville, Md.], 1.0 mg/L of amphotericin B [Fungizone®, E. R. Squibb & Sons,
30 Princeton, N.J.], and 2% FBS). Following incubation at 37°C for 7 days, a second 2-ml

agarose overlay containing 80 µg/ml of neutral red vital stain (GIBCO-BRL) was added.

Construction of recombinant DEN-2 16681/PDK-53 viruses

- 5 During the genetic validation of clone-derived DEN-2 viruses in the present study, two cDNA cloning errors were discovered, nt-6665 A-to-G (NS4A-97 Tyr-to-Cys) and nt-8840 A-to-G (NS5-424 Glu-to-Gly), in the previously reported PDK-53 virus-specific pD2/IC-130Vc-K (NS3-250-Val variant) clone (Kinney et al., Virology 230: 300-308 (1997)). These defects were corrected in a newly derived PDK-53 virus-specific (NS3-250-Val variant) clone, pD2/IC-VV45R.
- 10

In preliminary studies, recombinant 16681/PDK-53 viruses containing PDK-53 virus-specific gene regions within the genetic background of 16681 virus were used to investigate the genetic loci involved in the attenuation markers of PDK-53 virus.

- 15 Analyses of these viruses indicated that the PDK-53 mutation at nt-57 in the 5'NC region and the amino acid mutations at NS1-53 (analyzed in a linked manner with the NS2A-181 mutation) and NS3-250 were the determinants of the PDK-53 virus-specific phenotype. The prM-29 mutation has little effect on virulence. Based upon sequence analysis and comparison, the 5'NC, NS1 and NS3 mutations were subjected to further
- 20 mutational analysis. The 5'NC mutation occurred in a possible stem structure. The NS1 and NS3 mutations both occurred at loci conserved in some flaviviruses. 14 recombinant pD2/IC- 16681/PDK-53 plasmids were constructed by exchanging cDNA fragments between pD2/IC-30P-A (16681 clone) and pD2/IC-VV45R (PDK-53 clone) at restriction enzyme sites SstI (preceding the T7 promoter), SalI (nt-165), SphI (nt-
- 25 1380), SpeI (nt-2370 and nt-3579), KpnI (nt-4493), XhoI (nt-5426), and XbaI (3' end of the clone). All recombinant plasmids were grown in *Escherichia coli*, strain XLI-blue, and were linearized at the unique XbaI site engineered at the 3' terminus of the cDNA. BHK-21 cells were transfected with transcribed viral RNA by the method of Liljestrom et al. (*J. Virology* 63: 4107-4113 (1991)).

30

The genotypes of the recombinant D2/IC-Px (where x = 5, 1, and/or 3 to indicate the incorporation of the parental [P in the virus designation] 16681 virus-specific 5'NC-57, NS1-53, and/or NS3-250 loci into the pD2/IC-VV45R [PDK-53] backbone) and D2/IC-Vx (where x indicates the reciprocal incorporation of the three
5 candidate PDK-53 vaccine [V in the virus designation] virus-specific loci within the pD2/IC-30P-A [16681] backbone) viruses are shown in Table 11. If the 5'NC, NS1, and NS3 loci are the primary determinants of the PDK-53 virus-specific phenotype, then the D2/IC-P5 and D2/IC-V13 viruses should be equivalent (cognate) because both viruses contain 5'NC-57-C, NS1-53-Asp, and NS3-250-Val. The cognate virus pairs
10 derived from reciprocal mutagenesis of the 16681 and PDK-53 virus-specific infectious clones are indicated in Table 11. To further investigate the prM-29 locus, we moved the prM-29-Asp locus of DEN-2 16681 virus into pD2/IC-VV45R and pD2/IC-P5 to derive recombinant D2/IC-Pp and -P5p viruses, respectively. Reciprocal recombinations yielded D2/IC-Vp and -V5p viruses.

15

Each clone-derived virus (transfected BHK-21 seed) was propagated once in LLC-MK₂ cells. The genotypes of all of the LLC-MK₂-1-passaged, recombinant 16681/PDK-53 viruses were confirmed by complete nucleotide sequence analyses of their genomes. Because all of the viruses had the expected nucleotide sequences, we
20 inferred that their cDNA clones were also correct. All of the clone-derived viruses contained the 16681 virus-specific nt-8571-C locus, which is the site of a silent mutation in PDK-53 virus. Direct sequencing of overlapping cDNA amplicons generated from DEN-2 viral genomic RNA using reverse transcriptase-polymerase chain reaction (RT-PCR) was used to determine the sequence of all but the termini of
25 the cDNA. The sequences of the 5'- and 3'-terminal 30 nucleotides of the genome were determined by direct sequencing of the infectious clone cDNA in plasmid pBRUC-139. The D2/IC- prefix is eliminated in the virus designations in Table 11 and the following text.

30

Characterization of the replication phenotypes of recombinant 16681/PDK-53 viruses.

Viruses were analyzed for plaque size, temperature sensitivity, and replication in LLC-MK₂ and C6/36 cells. Plaque sizes were evaluated after 9 days of incubation under agarose in LLC-MK₂ cell monolayers grown in 6-well plates. Viral growth curves were performed in 75-cm² flasks of LLC-MK₂ or C6/36 cells inoculated at multiplicity of infection (m.o.i.) of approximately 0.001 PFU/cell. After adsorption at 37°C for 2 h, 30 ml of DMEM medium (LLC-MK₂ cells) or overlay nutrient medium (C6/36 cells) containing penicillin/streptomycin and 5% FBS was added, and the cultures were incubated in 5% CO₂ at 37°C or 29°C, respectively. Aliquots of culture medium were removed at 48-h intervals, adjusted to 12.5% FBS, and stored at -80°C prior to virus titration.

Temperature sensitivity assays were performed in LLC-MK₂ cells grown in 75-cm² flasks. The cells were inoculated at a m.o.i. of about 0.001 PFU/cell. After adsorption for 2 h at 37°C, 30 ml of DMEM medium containing 5% FBS was added. One set of cultures was incubated for 8 days at 37°C, the other at 38.7°C. The ratio of virus titer at 38.7°C versus the titer at 37°C was calculated.

Mouse neurovirulence assay

Litters of newborn, outbred white ICR mice were inoculated intracranially with 10⁴ PFU of virus in a volume of 30 µl. Mice were individually weighed once a week and were observed for paralysis or death for 35 days.

Plaque phenotypes of recombinant 16681/PDK-53 viruses

Mean diameters of virus plaques (n=12) at 9 days after infection under agarose overlay in LLC-MK₂ cells were measured (FIG. 4). The largest plaques (3.2-3.4 mean diameter) were produced by the wild-type 16681 virus, its clone-derived 30P-A virus,

and the recombinant P513 virus, which contained the 5'NC, NS1, and NS3 16681 virus-specific loci in the VV45R (PDK-53) virus genetic background (Table 11). These three 16681-specific loci within the PDK-53 genetic background were sufficient to reconstitute the large plaque phenotype of the 16681 virus.

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Individual PDK-53 virus-specific 5'-NC-57-T, NS1-53-Asp, and NS3-250-Val mutations incorporated into the 16681 genotype each resulted in significantly ($p < 0.00003$) decreased plaque sizes of 2.1-2.3 mm in V5, V1, and V3 viruses, respectively, versus those of 16681 virus. The plaque phenotypes of P13 and P51 viruses were
10 similar to those of their cognate V5 and V3 viruses (indicated by graph bars with identical solid or cross-hatching pattern in FIG. 4). The 2.8-mm plaque size of P53 virus differed from 16681 viral plaques to a lesser degree ($p < 0.03$) than did the 2.1-mm plaques of its cognate V1 virus. The 1.1 - 1.6-mm plaques of cognate virus pairs V13 (P5) (containing PDK-53 virus-specific NS1 and NS3 loci), V53 (P1) (PDK-53
15 virus-specific 5'NC and NS3 loci), and V51 (P3) virus (PDK-53 virus-specific 5'NC and NS1 loci) were essentially equivalent to the 1.3-mm plaques of PDK-53 virus. These results indicate that all pairwise combinations of these three PDK-53 virus-specific loci in the 16681 backbone generated a small-plaque virus similar to PDK-53 virus. Although V51 virus produced a plaque phenotype that was similar to that of
20 PDK-53 virus, all three 16681 virus-specific 5'NC-C, NS1-53-Gly, and NS3-250-Glu loci were required within the PDK-53 background of P513 virus to reconstitute the plaque phenotype of 16681 virus. The presence of all three PDK-53 loci in the 16681 backbone generated V513 virus, which had a smaller ($p < 0.001$, Student's *t* test) plaque phenotype than that of either PDK-53 or VV45R virus. The difference between
25 the plaque size of PDK-53 virus and that of VV45R virus was not significant.

Recombinant Vp virus, which contained the PDK-53 virus-specific prM-29-Val locus in the 16681 background, had a significantly ($p < 0.002$) reduced plaque size of 2.6 mm. However, the 1.0-mm plaque phenotype of Pp virus (16681 prM-29-Asp
30 locus in the PDK-53 background) was essentially identical to the 1.1-mm and 1.3-mm

plaques of VV45R and PDK-53 viruses (FIG. 4A), respectively. The prM-29 locus did not affect the plaque phenotypes of P5p (1.0 ± 0.0 mm) and V5p (2.0 ± 0.4 mm) viruses, which produced plaques similar to those of P5 (1.1 ± 0.3 mm) and V5 (2.3 ± 0.4 mm), respectively.

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Replication of recombinant 16681/PDK-53 viruses in LLC-MK₂ and C6/36 cells

All of the viruses replicated well in LLC-MK₂ cells, reaching peak titers of $10^{7.3}$ - $10^{7.9}$ PFU/ml at 6-8 days after infection. PDK-53 and its clone-derived VV45R virus replicated at a reduced rate during the first four days after infection, relative to the other
10 viruses. To determine temperature sensitivities, virus-infected LLC-MK₂ cells were incubated at 37°C or 38.7°C in 2-5 experiments (FIG. 4B). Temperature sensitivity scores were determined at 8 days after infection. All of the viruses exhibited some degree of temperature sensitivity under these conditions. In individual experiments, wild-type 16681 virus showed 75-80% titer reduction at 38.7°C. Virus V1 and cognate
15 viruses P3 (V51), which showed 84-86% average reductions in titer, were slightly more temperature-sensitive than 16681 virus. However, only PDK-53, VV45R, V513, P5p, Pp, and the cognate recombinant viruses V13 and P5, all of which contained both the NS1-53-Asp and NS3-250-Val PDK-53 virus- specific loci, reproducibly showed 90-97% average reduction in titer at 38.7°C.

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The 16681 virus and its clone-derived 30P-A virus replicated to average peak titers of $10^{8.6}$ - $10^{8.8}$ PFU/ml at 12 days after infection in two independent growth-curve experiments in C6/36 cells (FIG. 4C). The replication of PDK-53 virus (peak titer of $10^{4.5}$ PFU/ml) and its clone- derived VV45R (peak titer of $10^{4.6}$ PFU/ml) virus was
25 approximately 15,000-fold less efficient in C6/36 cells. The 16681 virus-specific 5'NC and NS1 loci within the PDK-53 background of P51 virus fully reconstituted the replication efficacy to that of wild-type 16681 virus. Conversely, the PDK-53 virus-specific 5'NC and NS1 loci within the 16681 background of V51 virus were sufficient to establish the crippled replication phenotype of PDK-53 virus. Recombinant cognate
30 virus pairs V5 (P13) and V1 (P53), which contained the PDK-53 virus- specific 5'NC

region or NS1 locus, respectively, replicated to average peak titers of $10^{5.9}$ - $10^{6.7}$ PFU/ml. Although the average peak titer of V53 virus was about 40-fold greater than that of V5 virus in C6/36 cells, the peak titers of P513, P13, P53, V3, V13, V513, and P3 viruses were very similar to those of P51, P1, P5, 30P-A, V1, V51, and VV45R viruses, respectively. These data indicated that the NS3-250 locus had little or no observable effect on replication in C6/36 cells (FIG. 4C). Vp and 16681 viruses had nearly equal average peak titers in C6/36 cells, as did P5 and P5p viruses. Pp and V5p viruses produced average peak titers that were slightly higher (8- and 40-fold, respectively) than those of PDK-53 and V5 viruses, respectively. The prM-29 locus appeared to have little or no effect on viral replication in C6/36 cells.

Neurovirulence of recombinant 16681/PDK-53 viruses in newborn mice

To investigate the neurovirulence of the recombinant viruses, two litters of newborn white ICR mice, eight mice per litter, were infected intracranially with 10^4 PFU of virus. The DEN-2 16681 virus and its clone-derived 30P-A virus cause 50%-100% mortality in these mice. Average survival times (AST) for mice succumbing to challenge with 16681 or 30P-A virus ranged from 15.2 to 16.8 days in various experiments. Mice were weighed individually every 7 days after infection. A single mouse died by day 1 after infection, presumably as a result of inoculation trauma, in each of the P53 and Vp groups (Table 12). These two mice were excluded from the analyses. There were no fatalities and no weight loss in the control, diluent-inoculated group.

Three mouse neurovirulence phenotypes were observed (Table 12). The first phenotype consisted of the mouse-virulent viruses DEN-2 16681, 30P-A, P513, P51, V3, and Vp, which caused at least 50% mortality with AST of 13.2-17.0 days (Table 12). In two other independent experiments, the Vp virus caused 46.67% mortality with AST of 17.4 ± 1.4 days ($n=16$) and 56.25% mortality with AST of 18.3 ± 1.3 days ($n=16$). In an independent experiment, P51 virus caused only 25% mortality with AST of 15.9 ± 5.5 days ($n=16$). A second phenotype consisted of the mouse-attenuated

PDK-53, VV45R, V513, Pp, and cognate V51 (P3) viruses, which caused no mortality, and the nearly attenuated V1, cognate V13 (P5), P5p, and V5p viruses, which killed only 1 of 16 mice (Table 12). The presence of the two PDK-53 virus-specific 5'NC-57-T and NS1-53-Asp loci within the 16681 genetic background was sufficient to result in
5 or maintain attenuation in cognate viruses V51 (P3). Except for P53 virus, all of the viruses containing the PDK-53 virus-specific NS1-53-Asp locus were attenuated or nearly attenuated.

The third phenotype, that of intermediate virulence, characterized cognate virus
10 pairs V5 (P13) and V53 (P1), and P53 virus which caused 18.75%-37.5% mouse mortality and significant weight loss ($p < 0.001$, Student's *t* test, at 3 weeks after infection, relative to diluent-inoculated control mice) in mice that survived virus challenge. Viruses V5 (P13) and V53 (P1) contained the 5'NC-57-T, but not the NS1-53-Asp, locus of PDK-53 virus. V1 virus (6.25% mortality) was more attenuated than
15 V5 virus, which produced 18.75% mortality and significant weight loss in the survivors. Conversely, the 16681 virus-specific 5'-NC-57-C locus caused little reversion to virulence in P5 virus (6.25% mortality), whereas the NS1-53-Gly moiety in P1 virus resulted in an intermediate level (37.5%) of mortality and significant weight loss in the survivors. Unlike the nearly attenuated cognate V1 virus, P53 virus had an
20 intermediate virulence phenotype. The NS1-53 locus had a more significant effect on the virulence phenotype than did the 5'-NC-57 locus.

The prM-29 locus showed no effect in P5p, Pp, and Vp viruses, relative to P5, PDK-53, and 16681 viruses, respectively. The V5p virus, which contained both PDK-
25 53 virus-specific 5'NC-57-T and prM-29-Val loci, was nearly attenuated (Table 2). The NS3-250 locus did not appear to contribute significantly to mouse neurovirulence phenotype in V3, P13, V53, V13, and P3 viruses, which exhibited phenotypes that were

equivalent to 16681, P1, V5, V1, and PDK-53 viruses, respectively. The difference in the level of mortality caused by P53 and P5 viruses suggested that the 16681 virus-specific NS3-250-Glu locus might contribute somewhat to the virulence phenotype within certain genetic contexts.

5

Evolution of mutations in the DEN-2 PDK-53 vaccine virus

Intermediate passages PDK-5, -10, -14, -35, and -45 of the 16681 virus were analyzed to determine the accrual of the nine nucleotide mutations in the PDK-53 vaccine strain. Amplicons were amplified directly from genomic mRNA extracted from the viral seed by RT/PCR. Automated sequencing of small genomic regions, which contained the nine relevant loci, was performed by using appropriate primers. The nucleotide residues identified at each of the nine loci for these viruses are shown in Table 13. The NS2A-181 Leu-to-Phe mutation and the silent mutations at E-37, NS3-342, and NS5-334 appeared by passage PDK-5 and were the predominant moieties by passage PDK-10 (NS2A-181), PDK-14 (E-373, NS3-342), or PDK-35 (NS5-334). Mutations 5'-NC-57 C-to-T, prM-29 Asp-to-Val, NS1-53 Gly-to-Asp, and NS4A-75 Gly-to-Ala occurred by passage PDK-35. The 5'-NC-57-T was predominant at passage PDK-35, while the other listed mutations became predominant by passage PDK-45. The NS3-250 Glu-to-Val mutation appeared by passage PDK-45 and is not fully mutated to the virus-specific Val in the current PDK-53 vaccine candidate (Table 13). Approximately 29% of the viral population in the PDK-53 vaccine contains NS3-250-Glu. The PDK-45 virus was genetically equivalent to the PDK-53 vaccine virus. In the present study, no attempt was made to determine the relative proportions of the two nucleotides at the mixed genetic loci shown in Table 13.

25

Example 6

Construction of chimeric DEN-2/West Nile clones and virus

Genome-length, chimeric DEN-2/WN infectious cDNA clones containing structural genes of WN virus within the genetic background of DEN-2 virus were

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constructed using the *in vitro* ligation strategy used to derive the chimeric DEN-2/3 viruses described earlier.

In a first example, the prM-E encoding cDNA of the 5'-end subclone that was
 5 used to derive a chimeric DEN-2/3-PP1 virus clone (see Example 2) was replaced with the prM-E gene region of WN virus, strain NY 99 (New York 1999). The cDNA fragment containing the prM-E gene region of WN virus was amplified by reverse transcriptase-polymerase chain reaction (RT-PCR) from WN virus-specific genomic RNA with forward primer WN-M
 10 (5'-GGAGCAGTTACCCTCTCTACGCGTCAAGGGAAGGTGATG-3' (SEQ ID NO:37); underlined MluI-site followed by WN virus sequence near the 5' end of the prM gene) and reverse primer cWN-E
 (5'-GAAGAGCAGAACTCCGCCCGCTGCGAGAAACGTGA GAGCTATGG-3' (SEQ ID NO:38); underlined NgoMIV site followed by sequence that was
 15 complementary to the WN genomic sequence near the 3' end of the E gene of WN virus). The amplified prM-E cDNA fragment was cloned into the MluI-NgoMIV sites of the intermediate pD2I/D3-P1-AscI clones, exactly as was done during the derivation of chimeric DEN-2/3 virus (see Example 2, construction of chimeric DEN-2/3 infectious clones), to replace the prM/E region of the DEN-3 16562 virus. In this
 20 chimeric DEN-2/WN cDNA, the prM splice site encoded the amino acid sequence (shown as single-letter amino acid abbreviations, and written in amino-to-carboxyl order) SAGMIIMLIPTVMA-FHLTTR**QGKVMMTV** (SEQ ID NO:39). The hyphen in this sequence indicates the polyprotein cleavage site located between the capsid and prM genes; the amino-terminal sequence is DEN-2 virus specific; the carboxyl-terminal
 25 sequence in bold, underlined, italicized font indicates the WN virus-specific sequence (QGKVMMTV) (SEQ ID NO:40) near the amino terminus of the prM protein encoded by this chimeric construct. This intermediate DEN-2/WN subclone was ligated *in vitro* with the 3'-end intermediate DEN-2 subclone, pD2-Pm^b-Asc, by the same protocol described in example 2 (construction of chimeric DEN-2/3 infectious clones) to
 30 produce the full genome-length, chimeric DEN-2/WN viral cDNA that was used to

transcribe chimeric DEN-2/WN virus-specific genomic RNA. Using the same protocol described in example 2, mammalian LLC-MK₂ or mosquito C6/36 cells were transfected with the transcribed chimeric DEN-2/WN RNA. This strategy, which involved using the same MluI restriction enzyme splice site that was used to derive the chimeric DEN-2/3 and DEN-2/4 viruses, failed to produce viable chimeric virus after transfection of the transcribed chimeric DEN-2/WN RNA in LLC-MK₂ cells, and resulted in only very low titers (< 100 PFU/ml) in C6/36 cells. This failure is probably due to significant gene sequence variation between the carboxyl-terminal ends of the viral capsid proteins and between the amino-terminal ends of the prM protein of DEN-2 and WN viruses. The carboxyl-terminal region of the flavivirus capsid protein serves as a signal peptide sequence for the insertion of prM into intracellular membranes (endoplasmic reticulum) during maturation and cleavage of the prM protein. This DEN-2/WN construct, which contained the capsid-carboxyl-terminal signal sequence, as well as the amino-terminal residues of the prM protein of the DEN-2 backbone, apparently did not permit appropriate maturation of the chimeric virus.

In a second example, the chimeric DEN-2/WN cDNA clone was modified so as to encode the carboxyl-terminal region of the capsid protein, as well as the entire prM protein and most of the E protein, of WN virus. A unique SstII restriction site was introduced by site-directed mutagenesis near the 3' terminus of the DEN-2 virus-specific capsid gene to serve as a new 5' splice site for the WN capsid-carboxyl-end/prM/E gene region. This SstII site introduced two silent mutations in the DEN-2 virus-specific sequence encoding the amino acid triad SAG (single-letter abbreviations). The appropriate gene region was amplified from WN viral RNA by using the forward primer WN-452.SAG (5'-AATTCAACGCGTACATCCGCGGGCACCGGAATTGCAGTCA TGATTGGCCTGATGGC-3' (SEQ ID NO:41); underlined SstII site followed by WN virus-specific sequence) and the same reverse cWN-E primer that was utilized in the previous construct (as described above). This amplified cDNA was cloned to make the intermediate subclone pDEN-2/WN-P-SA which contained cDNA encoding the 5'

noncoding region and most of the capsid gene from DEN-2 16681 virus and the carboxyl-terminal capsid, entire prM, and most of the E gene from WN virus, as well as a unique AscI site downstream of the NgoMIV site. In this chimeric DEN-2/WN cDNA, the prM splice site encoded the amino acid sequence (shown as single-letter amino acid abbreviations, and written in amino-to-carboxyl order)

5 SAG***TGLI*AVMIGLIASVGA-VTLSN***FQ***GKVMMTV** (SEQ ID NO:42). The hyphen in this sequence indicates the polyprotein cleavage site located between the capsid and prM genes; the amino-terminal sequence is DEN-2 virus specific; the carboxyl-terminal sequence in bold, underlined, italicized font indicates the WN virus-specific sequence

10 (TGLI***AVMIGLIASVGA-VTLSN***FQ***GKVMMTV***) (SEQ ID NO:43) encoded by this chimeric construct. Following the *in vitro* ligation protocol of the chimeric DEN-2/3 clones described for chimeric DEN-2/3 virus in example 2, the 5'-end intermediate subclone pDEN-2/WN-P-SA was ligated to the 3'-end pD2-Pm^ab-Asc subclone to produce the full genome-length cDNA of the chimeric DEN-2/WN-PP1 virus for

15 transcription of the chimeric RNA. The chimeric DEN-2/WN-PP1 construct encoded the indicated WN structural gene region within the genetic background of the wild-type DEN-2 16681 virus. Both LLC-MK₂ and C6/36 cells were transfected with RNA transcribed from this *in vitro*-ligated, chimeric DEN-2/WN-PP1 clone. Viable, chimeric DEN-2/WN-PP1 virus, at virus titers of 10³-10⁶ PFU/ml of culture medium,

20 was successfully recovered from both transfected cell cultures. Nucleotide sequence analysis of the entire genome of the clone-derived, chimeric DEN-2/WN virus demonstrated the expected genomic sequence. These results demonstrate that the DEN-2 infectious clones of the invention can be used to construct chimeric viruses that express structural genes of heterologous flaviviruses other than DEN-1, DEN-3, and

25 DEN-4 viruses.

All of the patents, publications and other references mentioned herein are hereby incorporated in their entirety by reference. Modifications and variations of the

present methods and compositions will be obvious to those skilled in the art from the foregoing detailed description. Such modifications and variations are intended to come within the scope of the appended claims.

Table 1

Viral Candidates for Flavivirus Chimeras[†]

<u>Primary Mosquito-</u>	<u>Other Mosquito-Borne:</u>	
<u>Borne Species</u>	<u>Species</u>	
Dengue-1 **	Alfuy	Jugra
Dengue-3 **	Bagaza	Kokobera
Dengue-4 **	Banzi **	Ntaya
Yellow fever **	Bouboui	Rocio **
Japanese encephalitis **	Bussuquara **	Sepik **
Murray Valley encephalitis **	Edge Hill **	Spondweni **
St. Louis encephalitis **	Ilheus	Stratford
West Nile **	Naranjal	Tembusu
Kunjin *	Israel turkey meningitis	Uganda S
		Usutu **
		Wesselsbron**
		Zika **
<u>Tick-Borne:</u>	<u>No Arthropod Vector Demonstrated</u>	
Absettarov **	Apoi *	
Gadgets Gully	Aroa	
Hanzalova **	Cacipacore	
Hypr **	Carey Island	
Kadam	Cowbone Ridge	
Karshi	Dakarbat **	
Kumlinge **	Entebbe bat	
Kyasanur Forest disease **	Jutiapa	
Langat	Koutango *	
Louping ill **	Modoc *	
Meaban	Montana Myotis leukemia	
Omsk hemorrhagic fever **	Negishi **	
Powassan **	Phnom-Penh bat	
Royal Farm	Rio Bravo **	
Russian spring	Saboya	
summer encephalitis **	Sal Vieja	
Saumarez Reef	San Perlita	
Tyuleny	Sokuluk	

* = Laboratory infection reported

** = Natural and laboratory infection reported

[†] = List includes the currently classified members of the *Flavivirus* genus in the International Catalogue of Arboviruses, Including Certain Other Viruses of Vertebrates, Nick Karabatsos, ed. The American Society of Tropical Medicine and Hygiene. 1985.

Table 2
Summary Of Nucleotide And Amino Acid Differences Between The Genomes Of
DEN-1 16007 Virus And Its Vaccine Derivative,
Strain PDK-13

Genome	<u>Nucleotide</u>		<u>Amino Acid</u>		<u>Protein</u>	<u>Polyprotein</u>
<u>Position</u>	<u>16007</u>	<u>PDK-13</u>	<u>16007</u>	<u>PDK-13</u>	<u>Position</u>	<u>Position</u>
1323	T	C	Val	Ala	E-130	410
1541)	G	A	Glu	Lys	E-203	483
1543)	A	G				
1545	G	A	Arg	Lys	E-204	484
1567	A	G	Gln	Gln	E-211	491
1608	C	T	Ser	Leu	E-225	505
2363	A	G	Met	Val	E-477	757
2695	T	C	Asp	Asp	NS1-92	867
2782	C	T	Ala	Ala	NS1-121	896
5063	G	A	Glu	Lys	NS3-182	1657
6048	A	T	Tyr	Phe	NS3-510	1985
6806	A	G	Met	Val	NS4A-144	2238
7330	A	G	Gln	Gln	NS4B-168	2412
9445	C	T	Ser	Ser	NS5-624	3117

Table 3
Summary Of Nucleotide And Amino Acid Sequence Differences Between The
Genomes Of DEN-2 16681 Virus And Its
Vaccine Derivative, Strain PDK-53

Genome	<u>Nucleotide</u>		<u>Amino Acid</u>		<u>Protein</u>	<u>Polypeptide</u>
<u>Position</u>	<u>16681</u>	<u>PDK-53</u>	<u>16681</u>	<u>PDK-53</u>	<u>Position</u>	<u>Position</u>
57	C	T ^a	-	-		
524	A	T	Asp	Val	prM-29	
2055	C	T	Phe	Phe	E-373	653
2579	G	A	Gly	Asp	NS1-53	828
4018	C	T	Leu	Phe	NS2A-181	1308
5270	A	T/A	Glu	Glu/Val ^b	NS3-250	1725
5547	T	C	Arg	Arg	NS3-342	1817
6599	G	C	Gly	Ala	NS4A-75	2168
8571	C	T	Val	Val	NS5-334	2825

^[a] 5' noncoding region.

^[b] The PDK-53 vaccine contains two genetic variants at nt-5270.

Table 4
Summary Of Nucleotide And Amino Acid Differences Between The Genomes Of
DEN-3 16562 Virus And Its Vaccine Derivative,
Strain PGMK-30/Frhl-3

<u>Genome</u>	<u>Nucleotide</u>		<u>Amino Acid</u>			
<u>Nucleotide</u>		PGMK-30	PGMK-30/	Protein	<u>Polyprotein</u>	
<u>Position</u>	<u>16562</u>	<u>FRhL-3</u>	<u>16562</u>	<u>FRhL-3</u>	<u>Position</u>	<u>Position</u>
550	C	T	Ala	Ala	prM-38	152
1521	C/T	C	Ser/Leu ^a	Ser	E-196	476
1813	G	A	Lys	Lys	E-293	573
1838	A	G	Ser	Gly	E-302	582
1913	G	A	Glu	Lys	E-327	617
2140	C	T	Ala	Ala	E-402	682
3725	T	C	Phe	Leu	NS2A-86	1211
4781	C	A	Gln	Lys	NS3-90	1563

^a Two significant genetic variants were located at nt-1521.

Table 5
Summary Of Nucleotide And Amino Acid Differences Between The
Genomes Of DEN-4 1036 Virus And Its Vaccine Derivative,
Strain PDK-48

<u>Genome</u>						
<u>Nucleotide</u>	<u>Nucleotide</u>		<u>Amino Acid</u>		<u>Protein</u>	<u>Polypeptide</u>
<u>Position</u>	<u>1036</u>	<u>PDK-48</u>	<u>1036</u>	<u>PDK-48</u>	<u>Position</u>	<u>Position</u>
1211	T	C	Ile	Ile	E-91	370
1971	G	A	Glu	Lys	E-345	624
3182	G	C	Gln	His	NS1-253	1027
6660	C	T	Leu	Phe	NS4A-95	2187
6957	A	A/T	Ile	Ile/Phe	NS4B-44	2286
7162	T	C	Leu	Ser	NS4B-112	2354
7546	C	C/T	Ala	Ala/Val	NS4B-240	2366
7623	G	T/G	Asp	Tyr/Asp	NS5-21	2508

Table 6
Summary Of Non-Silent Mutations Between The Genomes Of The Parent-
Vaccine Strains Of DEN-1, DEN-2, DEN-3, And DEN-4 Viruses

<u>Genome</u> <u>Nucleotide</u> <u>Position</u>	<u>DEN-1</u>	<u>DEN-2</u>	<u>DEN-3</u>	<u>DEN-4</u>
57		5'NC-57 c-t		
524		prM-29 D-V		
1323	E-130 V-A			
1521			E-196 S/L-S	
1541)	E-203 E-K			
1543)				
1545	E-204 R-K			
1608	E-225 S-L			
1838			E-302 S-G	
1913			E-327 E-K	
1971				E-345 E-K
2363	E-477 M-V			
2579		NS1-53 G-D		
3182				NS1-253 Q-H
3725			NS2A-86 F-L	
4018		NS2A-181 L-F		
4781			NS3-90 Q-K	
5063	NS3-182 E-K			
5270		NS3-250 E-V/E		
6048	NS3-510 Y-F			
6599		NS4A-75 G-A		
6660				NS4A-95 L-F
6806	NS4A-144 M-V			
6957				NS4B-44 I-I/F
7162				NS4B-112 L-S
7546				NS4B-240 A-A/V
7623				NS5-21 D-D/Y

Table 7
Immunogenicity of viruses in mice.
Plaque reduction-neutralization titer^a against DEN-1 16007 virus

	Experiment 1^b		Experiment 2^b	
	Primary	Boost	Primary	Boost
	Immunizing Pooled sera virus (Range)	Pooled sera (Range)	Pooled sera (Range)	Pooled sera (Range)
DEN-1 16007	80 (20 - 80)	2560 (80 - 20480)	80 (20 - 160)	2560 (160 - 5120)
D2/1-PP	80 ^c	5120 ^c	40 (10 - 160)	5120 (160 - 10240)
D2/1-EP	80 (20 - 320)	10240 (640 - 20480)	160 (20 - 320)	5120 (2560 - ≥10240)
D2/1-VP	40 (10 - 160)	2560 (160 - 5120)	80 (10 - 320)	5120 (40 - ≥10240)
DEN-1 PDK-13	10 (10 - 40)	80 ^c	40 (20 - 80)	320 (20 - 640)
D2/1-PV	10 (<10 ^d - 20)	80 ^c	40 (10 - 80)	2560 (20 - ≥10240)
D2/1-EV	20 (<10 ^d - 20)	80 ^c	40 (<10 ^d - 40)	160 (10 - 320)
D2/1-VV	10 (10 - 40)	80 ^c	40 (10 - 160)	160 (20 - 640)

^a Titers are the reciprocal dilution yielding at least 50% plaque reduction.

^b 3-week-old outbred ICR mice were immunized intraperitoneally with 10⁴ PFU of virus, and were boosted with the same virus dose 3 weeks later in experiment 1, or 6 weeks later in experiment 2. Primary = serum taken 20 days (experiment 1) or 41 days (experiment 2) after primary immunization. Boost = serum taken 21 days after boost in both experiments.

^c Individual titers were not determined.

^d Only one mouse serum titer was less than 10 in these groups.

^e Bold titers indicate the pooled sera titers were 4 fold higher than the titers calculated with 70% plaque reduction. All other pooled titers were either no different from or two fold higher than 70% plaque reduction titers.

Table 8
Neutralization of chimeric DEN viruses by standard antibodies

<u>Virus</u>	<u>Antibody</u>					
	<u>D1-AF^a</u>	<u>D2-AF^a</u>	<u>D2-H5^b</u>	<u>D3-AF^a</u>	<u>D3-8A1^b</u>	<u>D4-AF^a</u>
DEN-1 16007 ^c	1280 ^d	40	20	40	< 20	20
DEN-2/1-EP ^c	2560	;	;	;	;	;
DEN-2 16681 ^c	80	2560>	40960	40	< 20	40
DEN-3 16562 ^c	80	160	40	1280	5120	40
DEN-2/3-EP1 ^c	;	;	;	2560	20480	;
DEN-4 1036 ^c	20	40	< 20	80	< 20	1280
DEN-2/4-EP1 ^c	;	;	;	;	;	2560

^a AF = DEN-1 (D1), DEN-2 (D2), DEN-3 (D3), and DEN-4 (D4) virus-specific mouse ascitic fluids (polyvalent antisera).

^b DEN-2 and DEN-3 virus-specific, envelope glycoprotein-specific (E-specific) monoclonal antibodies D2-H5 and D3-8A1, respectively.

^c Wild-type DEN virus.

^d Reciprocal serum dilution-plaque reduction neutralization titers (50% endpoint) are shown;

; = not tested

^e Chimeric DEN-2/1-EP, DEN-2/3-EP1, or DEN-2/4-EP1 virus expressing structural genes of DEN-1 16007, DEN-3 16562, or DEN-4 1036 virus, respectively.

Table 9
Neurovirulence of chimeric DEN-2/3 and DEN-2/4 viruses in newborn
white ICR mice

<u>Challenge Virus^a</u>	<u>Percent Mortality^b</u>	<u>AST (SD) (days)^c</u>
DEN-3 16562 ^d	100.0	14.1 (2.1)
DEN-3 P30/FRhL-3 ^e	15.0	16.2 (3.2)
DEN-2/3-PP1 ^f	32.5	19.0 (2.1)
DEN-2/3-EP1 ^f	0.0	-
DEN-2/3-VP1 ^f	0.0	-
DEN-4 1036 ^d	100.0	8.6 (0.6)
DEN-4 PDK-48 ^e	100.0	10.7 (1.5)
DEN-2/4-PP1 ^f	62.5	17.8 (2.8)
DEN-2/4-EP1 ^f	0.0	-
DEN-2/4-VP1 ^f	0.0	-
DEN-2 16681 ^d	87.5	15.2 (2.6)
DEN-2 PDK53-E48 ^e	0.0	-
DEN-2 PDK53-V48 ^e	0.0	-
Diluent	0.0	-

^a Newborn mice were challenged intracranially with 10⁴ PFU of virus.

^b {Number of fatalities / total number (n=16) of mice challenged} x 100.

^c Average survival time (AST) and standard deviation (SD); - = not applicable, because there were no fatalities in this group.

^d Wild-type DEN serotype virus

^e Mahidol candidate DEN vaccine virus: DEN-3 = PGMK-30/FRhL-3 (P30/FRhL-3); DEN-4 = PDK-48; DEN-2 = PDK-53-E variant (NS3-250-Glu locus) and PDK-53-V variant (NS3-250-Val locus). Both PDK-53-E and -V variant viruses were derived from infectious cDNA clones of the variants.

^f Chimeric DEN-2/3 or DEN-2/4 virus. The prM/E gene region of DEN-3 16562 virus or DEN-4 1036 virus was expressed in the genetic background of wild-type DEN-2 16681 virus (PP1 viruses), Mahidol candidate vaccine DEN-2 PDK-53-E variant (EP1 viruses), or Mahidol candidate vaccine DEN-2 PDK-53-V variant (VP1 viruses).

Table 10

Protective efficacy of chimeric DEN-2/1 viruses in AG-129 mice^a

Reciprocal neutralizing antibody titer against appropriate homologous DEN-3 or DEN-4 virus at 4 or 6 weeks after immunization

<u>Immunizing Virus</u>	<u>4 weeks</u>	<u>6 weeks</u>
DEN-3 16562 ^b	320 ^c	640
DEN-3 P30/FRhL-3 ^d	160	320
DEN-2/3-EP1 ^e	80	320
DEN-4 1036 ^b	160	1280
DEN-4 PDK-48 ^d	80	320
DEN-2/4-EP1 ^e	20	40

^a AG-129 mice are an inbred strain that lack receptors for interferon alpha/beta and interferon gamma. Mice, 3.5 - 4.5 weeks in age, were immunized intraperitoneally with 10⁵ PFU of virus.

^b Wild-type DEN virus.

^c Reciprocal dilution of pooled serum that neutralized 70% or greater of the input wild-type DEN-3 16562 virus that was used to test sera from mice immunized with DEN-3 or chimeric DEN-2/3-EP1 virus, or the input wild-type DEN-4 1036 virus that was used to test sera from mice immunized with DEN-4 or chimeric DEN-2/4-EP1 virus.

^d Mahidol candidate vaccine virus, DEN-3 PGMK-30/FRhL-3 (P30/FRhL-3), DEN-4 PD-48.

^e Chimeric DEN-2/3-EP1 or DEN-2/4-EP1 expressing the prM/E gene region of DEN-3 16562 or DEN-4 1036 virus, respectively.

Table 11

Genotypes of recombinant DEN-2 16681/PDK-53 viruses

Clone-derived	<u>Dengue-2 16681 determinants in PDK-53 background^a</u>					
<u>virus (cognate)^b</u>	<u>5'NC-57</u>	<u>prM-29</u>	<u>NS1-53</u>	<u>NS2A-181</u>	<u>NS3-250</u>	<u>NS4A-75</u>
DEN-2 PDK-53	t	V	D	F	V	A
VV45R (V513)
P5 (V13)	c
P1 (V53)	.	.	G	.	.	.
P3 (V51)	E	.
P51 (V3)	c	.	G	.	.	.
P53 (V1)	c	.	.	.	E	.
P13 (V5)	.	.	G	.	E	.
P513 (30P-A)	c	.	G	.	E	.

	<u>Dengue-2 PDK-53 determinants in 16681 background^c</u>					
	<u>5'NC-57</u>	<u>prM-29</u>	<u>NS1-53</u>	<u>NS2A-181</u>	<u>NS3-250</u>	<u>NS4A-75</u>
DEN-2 16681	c	D	G	L	E	G
30P-A (P513)
V5 (P13)	t
V1 (P53)	.	.	D	.	.	.
V3 (P51)	V	.
V51 (P3)	t	.	D	.	.	.
V53 (P1)	t	.	.	.	V	.
V13 (P5)	.	.	D	.	V	.
V513 (VV45R)	t	.	D	.	V	.

^a The genome of the candidate dengue-2 PDK-53 vaccine virus differs from that of its 16681 parent at nine nucleotide loci, including three silent mutations (not shown), a mutation at genome nucleotide position 57 in the 5' noncoding region (5'NC-57; lower case letters), and five nucleotides encoding amino acid mutations (upper case, single-letter abbreviations) at viral polypeptide positions premembrane (prM)-29, nonstructural protein 1 (NS1)-53, NS2A-181, NS3-250, and NS4A-75 (32). Genetic loci from the parental 16681 virus were engineered into the cDNA background of the PDK-53 virus-specific infectious clone, pD2/IC-VV45R. Dots indicate sequence identity with PDK-53 virus (NS3-250-Val variant). The candidate PDK-53 vaccine also contains a genetic variant that has Glu at NS3-250 (32).

^b The genotypes of wild-type DEN-2 16681 virus, its attenuated vaccine derivative, DEN-2 PDK-53 virus, infectious clone-derived VV45R (genetically equivalent to the PDK-53 NS3-250-Val variant) and 30P-A (equivalent to wild-type 16681) viruses, and recombinant 16681/PDK-53 viruses are shown. The numerical designations for recombinant Px and Vx viruses (where x = 5'NC, NS1, and/or NS3 loci) indicate parental (P in virus designation) 16681 virus-specific loci engineered into the PDK-53 virus-specific infectious cDNA clone (top series) or reciprocal candidate PDK-53 vaccine (V in virus designation) virus-specific loci engineered into the 16681 clone (bottom series), respectively. P5 and V13 are cognate viruses, assuming that the PDK-53 virus-specific phenotype is determined predominantly by the 5'NC-57, NS1-53, and NS3-250 loci. Both P5 and V13 viruses contain the 5'NC-57-c, NS1-53-Asp, and NS3-250-Val loci within the genetic backgrounds of PDK-53 and 16681 viruses, respectively.

^c Genetic loci from PDK-53 virus were engineered into the cDNA background of the 16681 virus-specific infectious clone, pD2/IC-30P-A. Dots indicate sequence identity with 16681 virus.

Table 12
Neurovirulence of DEN-2 16681, PDK-53, and recombinant 16681/PDK-53 viruses
in newborn white ICR mice

<u>Mouse challenge^a</u>			<u>Virus genotype^b</u>					
	Mortality	AST (SD)	5'-NC	prM	NS1	NS2A	NS3	NS4A
<u>Virus (cognate)^c</u>	<u>(%)</u>	<u>(days)</u>	<u>57</u>	<u>29</u>	<u>53</u>	<u>181</u>	<u>250</u>	<u>75</u>
DEN-2 16681	68.75	15.2 (1.2)	c	D	G	L	E	G
30P-A (P513)	81.25	14.6 (2.3)
P513 (16681)	100.0	13.2 (1.6)	.	V	.	F	.	A
P51 (V3)	50.0 ^d	15.9 (5.5)	.	V	.	F	V	A
P1 (V53)	37.5 ^d	19.0 (4.2)	t	V	.	F	V	A
P13 (V5)	37.5 ^d	13.5 (2.1)	t	V	.	F	.	A
P53 (V1)	20.0 ^d	17.0 (7.8)	.	V	D	F	.	A
P5p (V13)	6.25	15.0	.	.	D	F	V	A
P5 (V13)	6.25	27.0	.	V	D	F	V	A
Pp (PDK-53)	0	- ^e	t	.	D	F	V	A
P3 (V51)	0	-	t	V	D	F	.	A
V3 (P51)	75.0 ^d	16.4 (3.2)	V	.
Vp (16681)	87.5	17.0 (0.9)	.	V
V53 (P1)	18.75 ^d	21.3 (6.1)	t	.	.	.	V	.
V5 (P13)	18.75 ^d	21.7 (4.2)	t
V5p (P13)	6.25	20.0	t	V
V13 (P5)	6.25	17.0	.	.	D	.	V	.
V1 (P53)	6.25	22.0	.	.	D	.	.	.
V51 (P3)	0	-	t	.	D	.	.	.
V513 (PDK-53)	0	-	t	.	D	.	V	.
VV45R (V513)	0	-	t	V	D	F	V	A
DEN-2 PDK-53	0	-	t	V	D	F	V	A

^a Percent mortality and average survival time (AST) \pm standard deviation (SD) of newborn, outbred white ICR mice challenged intracranially with 10^4 PFU of virus. Sixteen mice per group, except for the P53 and Vp groups in which a single mouse died by day 1 after infection, presumably as a result of inoculation trauma. These two mice were excluded from the study.

^b See text for explanation of virus genotypes. Solid dots indicate sequence identity with 16681 virus.

^c See text for explanation of virus and cognate virus designations.

^d Mean body weight of surviving mice was significantly lower ($p < 0.001$, Student's *t* test) than that of diluent-inoculated control mice (not shown) at 3 weeks after infection.

^e Average survival time is not applicable because there was no mortality in this mouse group.

Table 13
Evolution of DEN-2 virus, vaccine strain PDK-53, during passage of the parental
16681 strain in primary dog kidney (PDK) cells

Genome nucleotide position ^a / Translated polypeptide position ^b / Encoded amino acids ^c									
	57 ^a	524	2055	2579	4018	5270	5547	6599	8571
		prM-29 ^b	E-373	NS1-53	NS2A-181	NS3-250	NS3-342	NS4A-75	NS5-334
<u>Virus</u>	<u>—</u>	<u>D - V^c</u>	<u>F - F</u>	<u>G - D</u>	<u>L - F</u>	<u>E - V</u>	<u>R - R</u>	<u>G - A</u>	<u>V - V</u>
16681	C ^d	A	C	G	C	A	T	G	C
PDK-5	C	A	C/T ^e	G	T/C	A	T/C	G	C/T
PDK-10	C	A	T/C	G	T	A	C/T	G	T/C
PDK-14	C	A	T	G	T	A	C	G	T/C
PDK-35	T	T/A	T	A/G	T	A	C	C/G	T
PDK-45	T	T	T	A	T	A/T	C	C	T
PDK-53	T	T	T	A	T	A/T	C	C	T

^a Genome nucleotide positions of the nine nucleotide sequence differences between 16681 and PDK-53 viruses. Nucleotide position 57 lies within the 5' noncoding region of the viral genome.

^b Protein designations are as follows: prM = premembrane protein; E = envelope glycoprotein; NS = nonstructural protein.

^c The virus-specific amino acid residues (16681 - PDK-53) are shown for each amino acid position.

^d A, C, G, and T (cDNA sense) nucleotides are indicated.

^e Two genetic populations were identified for this locus in the virus. The order of the two nucleotides reflects relative peak heights of the nucleotide signals in sequence chromatograms.

Table 14

**Conservation of DEN-2 PDK-53 phenotypic attenuation markers
in chimeric DEN viruses.**

<u>Attenuation phenotype</u>	<u>DEN virus</u>			
	<u>DEN-2^a</u>	<u>DEN-2/1</u>	<u>DEN-2/3</u>	<u>DEN-2/4</u>
Attenuation in mice	+	+	+	+
Decreased replication in C6/36 cells	+	+	+	+
Small plaques in LLC-MK ₂ cells	+	+	+	+
Temperature sensitivity in LLC-MK ₂ cells	+	+	+	+

^a Mahidol candidate DEN-2 PDK-53 vaccine virus. The chimeric DEN-2/1, DEN-2/3, and DEN-2/4 viruses were constructed in the DEN-2 PDK-53 genetic background, NS3-250-Val or -Glu variant. The phenotypes shown for chimeric viruses are representative of chimeric viruses constructed in the background of either variant of DEN-2 PDK-53 virus.

Table 15

**Diagnostic Genetic Probes and Amplimers for the Candidate Mahidol
DEN-1, DEN-2, DEN-3, and DEN-4 Vaccine Viruses.**

Genetic Locus: D1V-1323 = Mutated genetic locus for candidate DEN-1 PDK-13
vaccine (V) virus at genome nucleotide position 1323.

Primer designations: p = TaqMan probe sequence, mRNA-sense
pc = TaqMan probe sequence, complementary-sense
f = forward amplimer, mRNA-sense
r = reverse amplimer, complementary-sense
SEQ ID = probe or primer sequence.

<u>Genetic Locus</u>	<u>Primer Designation</u>	<u>SEQ ID NO:</u>
D1V-1323		
Probe	pcD1V-1308	44
F	fD1V-1298	45
R	rD1V-1347	46
D1V-1541, 1543, 1545		
Probe	pcD1V-1530	47
F	fD1V-1519	48
R	rD1V-1567	43
D1V-1567		
Probe	pD1V-1580	50
F	fD1V-1545	51
R	rD1V-1608	52
D1V-1608		
Probe	pcD1V-1595	53
F	fD1V-1567	54
R	rD1V-1626	55
D1V-2363		
Probe	pD1V-2374	56
F	fD1V-2334	57
R	rD1V-2386	58
D1V-2695		
Probe	pcD1V-2686	59
F	fD1V-2660	60
R	rD1V-2735	61
D1V-2782		
Probe	pD1V-2767	62
F	fD1V-2752	63
R	rD1V-2801	64

Table15 (continued)

**Diagnostic Genetic Probes and Amplimers for the Candidate Mahidol
DEN-1, DEN-2, DEN-3, and DEN-4 Vaccine Viruses.**

<u>Genetic Locus</u>	<u>Primer Designation</u>	<u>SEQ ID NO:</u>
D1V-5063		
Probe	pcD1V-5052	65
F	fd1V-5040	66
R	rd1V-5095	67
D1V-6048		
Probe	pD1V-6059	68
F	fd1V-6030	69
R	rd1V-6069	70
D1V-6806		
Probe	pcD1V-6793	71
F	fd1V-6780	72
R	rd1V-6825	73
D1V-7330		
Probe	pD1V-7343	74
F	fd1V-7310	75
R	rd1V-7351	76
D1V-9445		
Probe	pcD1V-9433	77
F	fd1V-9419	78
R	rd1V-9485	79
D2V-57		
Probe	pD2V-69	80
F	fd2V-32	81
R	rd2V-81	82
D2V-524		
Probe	pcD2V-513	83
F	fd2V-492	84
R	rd2V-551	85
D2V-2055		
Probe	pD2V-2067	86
F	fd2V-2025	87
R	rd2V-2080	88
D2V-2579		
Probe	pcD2V-2568	89
F	fd2V-2535	90
R	rd2V-2603	91

Table15 (continued)

**Diagnostic Genetic Probes and Amplimers for the Candidate Mahidol
DEN-1, DEN-2, DEN-3, and DEN-4 Vaccine Viruses.**

<u>Genetic Locus</u>	<u>Primer Designation</u>	<u>SEQ ID NO:</u>
D2V-4018		
Probe	pD2V-4030	92
F	fD2V-3993	93
R	rD2V-4043	94
D2V-5270-E		
D2V-5270-V		
ProbeE	pD2VE-5279	95
ProbeV	pD2VV-5279	96
F	fD2V-5243	97
R	rD2V-5295	98
D2V-5547		
Probe	pD2V-5558	99
F	fD2V-5521	100
R	rD2V-5589	101
D2V-6599		
Probe	pcD2V-6588	102
F	fD2V-6569	103
R	rD2V-6625	104
D2V-8571		
Probe	pD2V-8582	105
F	fD2V-8535	106
R	rD2V-8594	107
D3V-550		
Probe	pD3V-562	108
F	fD3V-525	109
R	rD3V-575	110
D3V-1521		
Probe	pD3V-1533	111
F	fD3V-1497	112
R	rD3V-1541	113
D3V-1813		
Probe	pcD3V-1804	114
F	fD3V-1767	115
R	rD3V-1838	116
D3V-1838		
Probe	pcD3V-1827	117
F	fD3V-1813	118
R	rD3V-1913	119

Table15 (continued)

**Diagnostic Genetic Probes and Amplimers for the Candidate Mahidol
DEN-1, DEN-2, DEN-3, and DEN-4 Vaccine Viruses.**

<u>Genetic Locus</u>	<u>Primer Designation</u>	<u>SEQ ID NO:</u>
D3V-1913		
Probe	pcD3V-1903	120
F	fd3V-1891	121
R	rd3V-1967	122
D3V-2140		
Probe	pcD3V-2127	123
F	fd3V-2116	124
R	rd3V-2188	125
D3V-3725		
Probe	pD3V-3738	126
F	fd3V-3698	127
R	rd3V-3745	128
D3V-4781		
Probe	pcD3V-4772	129
F	fd3V-4762	130
R	rd3V-4801	131
D4V-1211 (T-C)		
Probe	pD4V-1222	132
F	fd4V-1191	133
R	rd4V-1250	134
D4V-1971 (G-A)		
Probe	pcD4V-1957	135
F	fd4V-1943	136
R	rd4V-2010	137
D4V-3182 (G-C)		
Probe	pD4V-3193	138
F	fd4V-3154	139
R	rd4V-3227	140
D4V-6660 (C-T)		
Probe	pcD4V-6648	141
F	fd4V-6638	142
R	rd4V-6688	143
D4V-7162 (T-C)		
Probe	pD4V-7174	144
F	fd4V-7141	145
R	rd4V-7188	146

Table 16

SEQ ID NO: for TaqMan probes and amplimers.

Underlined residues indicate the positions of the candidate vaccine virus mutation within the primer sequence, or, in the case of SEQID #52, the underlined residue indicates the nt-5270 position of DEN-2 16681 virus.

SEQ ID NO:

44	5'-TTCATATTGAGCTATCTTTCCTTCTA-3'
45	5'-GTGTGCCAAGTTTAAGTGTG-3'
46	5'-TGGACGGTGACTATCACTG-3'
47	5'-AAGCCATGATTTCTTTTCATTGTCA-3'
48	5'-CAGGGCTAGATTTTAACGAG-3'
49	5'-AGTGGTAAGTCTAGAAACCAC-3'
50	5'-TCCACAAACAGTGGTTTCTAGACT-3'
51	5'-TGTTGCTGACAATGAAAAAGAA-3'
52	5'-TCCAAGTCTCTTGGGATGTTA-3'
53	5'-TGGGATGTTAAAGCCCCAGAGGT-3'
54	5'-TCATGGCTTGTCCACAAACAG-3'
55	5'-CCAGTAAATCTTGTCTGTTCC-3'
56	5'-CGTCCCTTTCGGTGATGTGCATC-3'
57	5'-ATTCTGCTGACATGGCTAGG-3'
58	5'-TCCTAGGTACAGTGTGACC-3'
59	5'-AGATTCCACTAACGTCTCCACG-3'
60	5'-AATTGAACCACATCCTACTTG-3'
61	5'-TTGTGTTCCATGGGTTGTGG-3'
62	5'-TATGATTTTAGCTTTTCCCCAGCTT-3'
63	5'-GCCACAACCCATGGAACAC-3'
64	5'-ATGAAGGTGGTGTCTGTAC-3'
65	5'-TCCTAAACACCTTGTCTCAATCT-3'
66	5'-GCTAAGGCATCACAAGAAGG-3'
67	5'-CGATCCTGGATGTAGGTCC-3'
68	5'-CAGCCCTCTTTGAGCCGGAGA-3'
69	5'-AATATAAACACACCAGAAGG-3'
70	5'-TCCCCGTCTATAGCTGCAC-3'
71	5'-TGTCAATATCACGAATAACAGACCT-3'
72	5'-CACAGGACAACCAGCTAGC-3'
73	5'-AATAATCCCATCTCATTGG-3'
74	5'-ATTTGAAAAACAGCTAGGCCAAATAA-3'
75	5'-CTTAGATCCCGTGGTTTACG-3'
76	5'-AATCTGTGATGTGCAAAGTATC-3'
77	5'-AAAGATTCCCTCAGACTCCATTTGT-3'
78	5'-CACTTTCACCAACATGGAGG-3'

Table 16 (continued)

SEQ ID NO: for TaqMan probes and amplimers.

79	5'-CGAGAACTCTTCCGGCTAG-3'
80	5'-AGCTAAGCTCAATGTAGTCTAACA-3'
81	5'-CGTGGACCGACAAAGACAG-3'
82	5'-TCATCAGAGATCTGCTCTCT-3'
83	5'-ATGTTACGCCAACCTCTGTTTAA-3'
84	5'-GATCGTCAGCAGACAAGAG-3'
85	5'-CAATTCACCAAGGTCCATGG-3'
86	5'-AACCTCCATTGGGAGACAGCTAC-3'
87	5'-AATTGTGACAGAAAAAGATAGC-3'
88	5'-TCAGTTGTCCCGGCTCTAC-3'
89	5'-ATTCCACAAATGTCCTCTTCATGG-3'
90	5'-TACAAGTTCCAACCAGAATCC-3'
91	5'-CATCAGATTCTCCAGTCTTG-3'
92	5'-TTTCCCCACTGTTCTTAACATCCT-3'
93	5'-GAAAGTGAGTTGCACAATATTG-3'
94	5'-ATGCTAATGGTATCCAATCTG-3'
95	5'-CATCAGAGCTGAGCACACCGG-3'
96	5'-CATCAGAGCTGTGCACACCGG-3'
97	5'-CCTTAGAGGACTTCCAATAAG-3'
98	5'-AATGTGGCATGACACATTAGG-3'
99	5'-ATCCCTGAACGCTCGTGGAATTC-3'
100	5'-AGAGCAATGCACCAATCATAG-3'
101	5'-GAACGAACCAAACAGTCTTC-3'
102	5'-TATGCCCCTTGCGCTCATCAAG-3'
103	5'-CACTTCTGGCTACAGTCAC-3'
104	5'-GTGATTATGCAGCACATTCC-3'
105	5'-CTTGGGACGTTGTCCCCATGGT-3'
106	5'-CAGCATCATCCATGGTCAAC-3'
107	5'-GGAGTCGTGTCTGTCATTG-3'
108	5'-CACTCATAGCTATGGATCTGGGA-3'
109	5'-CTTTTCAAGACAGCCTCTGG-3'
110	5'-CATTTGTAAGTGACCGTGTC-3'
111	5'-CAATGAAATGATCTCATTGACAATGAA-3'
112	5'-AATGCTCACCACGGACAGG-3'
113	5'-TTGTCTATGTACCATCCATGC-3'
114	5'-CATAGCTCATCCCTTTGAGTTCC-3'
115	5'-GAGGCACAAGTATCTTTGC-3'
116	5'-TTTCTTCAACACAAAGCTACC-3'
117	5'-ACACAAAGCTACCAAGCACATTG-3'
118	5'-GATGGACAAATTGGAAGTCAAA-3'
119	5'-ATCTTGCAGGGTGCATCTTT-3'

Table 16 (continued)

SEQ ID NO: for TaqMan probes and amplimers.

120 5'-AGGGTGCATCTTTCCCTTTGTAC-3'
121 5'-GCAGCATGGGACAATACTC-3'
122 5'-GTGATCAGTCTGCCATTGTG-3'
123 5'-CCTCTGGCAGTAGCCTCGAACATCT-3'
124 5'-ACTGGTACAAGAAGGGAAGC-3'
125 5'-ACCCACTGATCCAAAGTCC-3'
126 5'-TCAGCCACTCCTGGCTTTGGG-3'
127 5'-GGCGTCACTTACCTAGCTC-3'
128 5'-TAGATGTCAGTTTCCTCAGG-3'
129 5'-CCTCCCCCTTTTTCCATTGTGC-3'
130 5'-TTTCATACGGAGGAGGATGG-3'
131 5'-AGGCTCTACGGCAATAACC-3'
132 5'-CAACAGTACATCTGCCGGAGAGA-3'
133 5'-GAGAGCCTTATCTAAAAGAGG-3'
134 5'-CTTTTCCAAACAAGCCACAG
135 5'-AACCACTTTTTTTCTTGTTACATCTC
136 5'-TGGAGCTCCGTGTAAAGTC-3'
137 5'-GCACTGTTGGTATTCTCAGC-3'
138 5'-CCCTTTTTTCACACCACAATTACCG-3'
139 5'-GAAAGCCAGATGCTCATTCC-3'
140 5'-TATCTCTAATTTGCCTAAGTGC-3'
141 5'-CTACCCAGAAACAAGCCACTAGC-3'
142 5'-ATTGTCAATGGGTTTGATAACC-3'
143 5'-TATGATTGAGGCCGCTATCC-3'
144 5'-TAGTCATGCTTTCAGTCCATTATGC-3'
145 5'-AGTGAACCCAACAACTTTGAC-3'
146 5'-TGGCTTTTGCCTGCAATCC-3'

We claim:

1. A nucleic acid chimera comprising a first nucleotide sequence encoding nonstructural proteins from an attenuated dengue-2 virus and a second nucleotide sequence encoding a structural protein from a second flavivirus.
2. The nucleic acid chimera of claim 1, wherein the attenuated dengue-2 virus is vaccine strain PDK-53.
3. The nucleic acid chimera of claim 2, wherein the structural protein is selected from the group consisting of a C protein of dengue-1 virus, a prM protein of dengue-1 virus, an E protein of dengue-1 virus or any combination thereof.
4. The nucleic acid chimera of claim 2, wherein the structural protein is selected from the group consisting of a C protein of dengue-2 virus, a prM protein of dengue-2 virus, an E protein of dengue-2 virus or any combination thereof.
5. The nucleic acid chimera of claim 2, wherein the structural protein is selected from the group consisting of a C protein of dengue-3 virus, a prM protein of dengue-3 virus, an E protein of dengue-3 virus or any combination thereof.
6. The nucleic acid chimera of claim 5, wherein the structural protein is an E protein of dengue-3 virus and the E protein contains a leucine at amino acid position 345.
7. The nucleic acid chimera of claim 2, wherein the structural protein is selected from the group consisting of a C protein of dengue-4 virus, a prM protein of dengue-4 virus, an E protein of dengue-4 virus or any combination thereof.

8. The nucleic acid chimera of claim 7, wherein the structural protein is an E protein of dengue-4 virus and the E protein contains a leucine at amino acid position 447, and further comprises a C protein of dengue-2 virus and the C protein contains a serine at position 100.
9. The nucleic acid chimera of claim 8, further comprising a valine at position 364 of the E protein.
10. The nucleic acid chimera of claim 2, wherein the structural protein is selected from the group consisting of a C protein of West Nile virus, a prM protein of West Nile virus, an E protein of West Nile virus or any combination thereof.
11. The nucleic acid chimera of claim 2, wherein the structural protein is selected from the group consisting of a C protein of Japanese encephalitis virus, a prM protein of Japanese encephalitis virus, an E protein of Japanese encephalitis virus or any combination thereof.
12. The nucleic acid chimera of claim 2, wherein the structural protein is selected from the group consisting of a C protein of St. Louis encephalitis virus, a prM protein of St. Louis encephalitis virus, an E protein of St. Louis encephalitis virus or any combination thereof.
13. The nucleic acid chimera of claim 2, wherein the structural protein is selected from the group consisting of a C protein of tick-borne encephalitis virus, a prM protein of tick-borne encephalitis virus, an E protein of tick-borne encephalitis virus or any combination thereof.
14. The nucleic acid chimera of claim 2, wherein the structural protein is selected from the group consisting of a C protein of yellow fever virus, a prM protein of yellow fever virus, an E protein of yellow fever virus or any combination thereof.

15. The nucleic acid chimera of claim 2, wherein the second flavivirus is a virulent strain.
16. The nucleic acid chimera of claim 15, wherein the structural protein is selected from the group consisting of a C protein of dengue-1 virus, a prM protein of dengue-1 virus, an E protein of dengue-1 virus or any combination thereof.
17. The nucleic acid chimera of claim 15, wherein the structural protein is selected from the group consisting of a C protein of dengue-2 virus, a prM protein of dengue-2 virus, an E protein of dengue-2 virus or any combination thereof.
18. The nucleic acid chimera of claim 15, wherein the structural protein is selected from the group consisting of a C protein of dengue-3 virus, a prM protein of dengue-3 virus, an E protein of dengue-3 virus or any combination thereof.
19. The nucleic acid chimera of claim 18, wherein the structural protein is an E protein of dengue-3 virus and the E protein contains a leucine at position 345.
20. The nucleic acid chimera of claim 15, wherein the structural protein is selected from the group consisting of a C protein of dengue-4 virus, a prM protein of dengue-4 virus, an E protein of dengue-4 virus or any combination thereof.
21. The nucleic acid chimera of claim 20, wherein the structural protein is an E protein of dengue-4 virus and the E protein contains a leucine at amino acid position 447, and further comprises a C protein of dengue-2 virus and the C protein contains a serine at position 100.
22. The nucleic acid chimera of claim 21, further comprising a valine at position 364 of the E protein.

23. The nucleic acid chimera of claim 15, wherein the structural protein is selected from the group consisting of a C protein of West Nile virus, a prM protein of West Nile virus, an E protein of West Nile virus or any combination thereof.

24. The nucleic acid chimera of claim 15, wherein the structural protein is selected from the group consisting of a C protein of Japanese encephalitis virus, a prM protein of Japanese encephalitis virus, an E protein of Japanese encephalitis virus or any combination thereof.

25. The nucleic acid chimera of claim 15, wherein the structural protein is selected from the group consisting of a C protein of St. Louis encephalitis virus, a prM protein of St. Louis encephalitis virus, an E protein of St. Louis encephalitis virus or any combination thereof.

26. The nucleic acid chimera of claim 15, wherein the structural protein is selected from the group consisting of a C protein of tick-borne encephalitis virus, a prM protein of tick-borne encephalitis virus, an E protein of tick-borne encephalitis virus or any combination thereof.

27. The nucleic acid chimera of claim 15, wherein the structural protein is selected from the group consisting of a C protein of yellow fever virus, a prM protein of yellow fever virus, an E protein of yellow fever virus or any combination thereof.

28. A nucleic acid chimera comprising a first nucleotide sequence encoding nonstructural proteins from an attenuated dengue-2 virus, and at least two different nucleotide sequences, each encoding a structural protein from at least two different flaviviruses.

29. The nucleic acid of claim 28, wherein the attenuated dengue-2 virus is vaccine strain PDK-53.

30. The nucleic acid chimera of claim 28, wherein the structural protein is selected from the group consisting of a C protein of dengue-1 virus, a C protein of dengue-2 virus, a C protein of dengue-3 virus, a C protein of dengue-4 virus, a prM protein of dengue-1 virus, a prM protein of dengue-2 virus, a prM protein of dengue-3 virus, a prM protein of dengue-4 virus, an E protein of dengue-1 virus, an E protein of dengue-2 virus, an E protein of dengue-3 virus, an E protein of dengue-3 virus containing a leucine at amino acid position 345, an E protein of dengue-4 virus, an E protein of dengue-4 virus containing a leucine at amino acid position 447, an E protein of dengue-4 virus containing a leucine at amino acid position 447 and a valine at amino acid position 364, a C protein of dengue-2 virus containing a serine at amino acid position 100 or any combination thereof.

31. The nucleic acid chimera of claim 28, wherein the at least two different flaviviruses are selected from the group consisting of the dengue-1 virus, dengue-2 virus, dengue-3 virus, dengue-4 virus, West Nile virus, Japanese encephalitis virus, St. Louis encephalitis virus, tick-borne encephalitis virus, yellow fever virus or any combination thereof.

32. A composition comprising one or more than one nucleic acid chimera of claim 1 and a pharmaceutically acceptable carrier.

33. The composition of claim 32, further comprising an immunizing composition selected from the group consisting of a dengue virus vaccine, a yellow fever virus vaccine, a tick-borne encephalitis virus vaccine, a Japanese encephalitis virus vaccine, a West Nile virus vaccine, a hepatitis C virus vaccine or any combination thereof.

34. A composition comprising one or more than one nucleic acid chimera of claim 28 and a pharmaceutically acceptable carrier.

35. The composition of claim 34, further comprising an immunizing composition selected from the group consisting of a dengue virus vaccine, a yellow fever virus vaccine, a tick-borne encephalitis virus vaccine, a Japanese encephalitis virus vaccine, a West Nile virus vaccine, a hepatitis C virus vaccine or any combination thereof.
36. A method of inducing an immune response in a subject comprising administering an effective amount of the composition of claim 32 to the subject.
37. A method of inducing an immune response in a subject comprising administering an effective amount of the composition of claim 33 to the subject.
38. A method of inducing an immune response in a subject comprising administering an effective amount of the composition of claim 34 to the subject.
39. A method of inducing an immune response in a subject comprising administering an effective amount of the composition of claim 35 to the subject.
40. An isolated nucleic acid consisting essentially of a nucleotide sequence of a genome of a dengue-2 virus, wherein the nucleotide sequence contains a mutation at position 2579 which results in the presence of an aspartate at amino acid residue 53 of the NS1 protein.
41. The nucleic acid of claim 40, wherein the nucleotide sequence further contains a mutation at position 57 which disrupts the function of the 5' noncoding region.
42. The nucleic acid of claim 40, wherein the nucleotide sequence further contains a mutation at position 5270 which results in the presence of a valine at amino acid residue 250 of the NS3 protein.

43. The nucleic acid of claim 42, wherein the nucleotide sequence further contains a mutation at position 57 which disrupts the function of the 5' noncoding region.

44. A nucleic acid chimera comprising the nucleotide sequence of claim 40 and a nucleotide sequence encoding a flavivirus structural protein selected from the group consisting of a C protein of dengue-1 virus, a prM protein of dengue-1 virus, an E protein of dengue-1 virus or any combination thereof.

45. A nucleic acid chimera comprising the nucleotide sequence of claim 40 and a nucleotide sequence encoding a flavivirus structural protein selected from the group consisting of a C protein of dengue-2 virus, a prM protein of dengue-2 virus, an E protein of dengue-2 virus or any combination thereof.

46. A nucleic acid chimera comprising the nucleotide sequence of claim 40 and a nucleotide sequence encoding a flavivirus structural protein selected from the group consisting of a C protein of dengue-3 virus, a prM protein of dengue-3 virus, an E protein of dengue-3 virus or any combination thereof.

47. A nucleic acid chimera comprising the nucleotide sequence of claim 40 and a nucleotide sequence encoding a flavivirus structural protein selected from the group consisting of a C protein of dengue-4 virus, a prM protein of dengue-4 virus, an E protein of dengue-4 virus or any combination thereof.

48. A nucleic acid chimera comprising the nucleotide sequence of claim 41 and a nucleotide sequence encoding a flavivirus structural protein selected from the group consisting of a C protein of dengue-1 virus, a prM protein of dengue-1 virus, an E protein of dengue-1 virus or any combination thereof.

49. A nucleic acid chimera comprising the nucleotide sequence of claim 41 and a nucleotide sequence encoding a flavivirus structural protein selected from the group consisting of a C protein of dengue-2 virus, a prM protein of dengue-2 virus, an E protein of dengue-2 virus or any combination thereof.

50. A nucleic acid chimera comprising the nucleotide sequence of claim 41 and a nucleotide sequence encoding a flavivirus structural protein selected from the group consisting of a C protein of dengue-3 virus, a prM protein of dengue-3 virus, an E protein of dengue-3 virus or any combination thereof.

51. A nucleic acid chimera comprising the nucleotide sequence of claim 41 and a nucleotide sequence encoding a flavivirus structural protein selected from the group consisting of a C protein of dengue-4 virus, a prM protein of dengue-4 virus, an E protein of dengue-4 virus or any combination thereof.

52. A nucleic acid chimera comprising the nucleotide sequence of claim 42 and a nucleotide sequence encoding a flavivirus structural protein selected from the group consisting of a C protein of dengue-1 virus, a prM protein of dengue-1 virus, an E protein of dengue-1 virus or any combination thereof.

53. A nucleic acid chimera comprising the nucleotide sequence of claim 42 and a nucleotide sequence encoding a flavivirus structural protein selected from the group consisting of a C protein of dengue-2 virus, a prM protein of dengue-2 virus, an E protein of dengue-2 virus or any combination thereof.

54. A nucleic acid chimera comprising the nucleotide sequence of claim 42 and a nucleotide sequence encoding a flavivirus structural protein selected from the group consisting of a C protein of dengue-3 virus, a prM protein of dengue-3 virus, an E protein of dengue-3 virus or any combination thereof.

55. A nucleic acid chimera comprising the nucleotide sequence of claim 42 and a nucleotide sequence encoding a flavivirus structural protein selected from the group consisting of a C protein of dengue-4 virus, a prM protein of dengue-4 virus, an E protein of dengue-4 virus or any combination thereof.

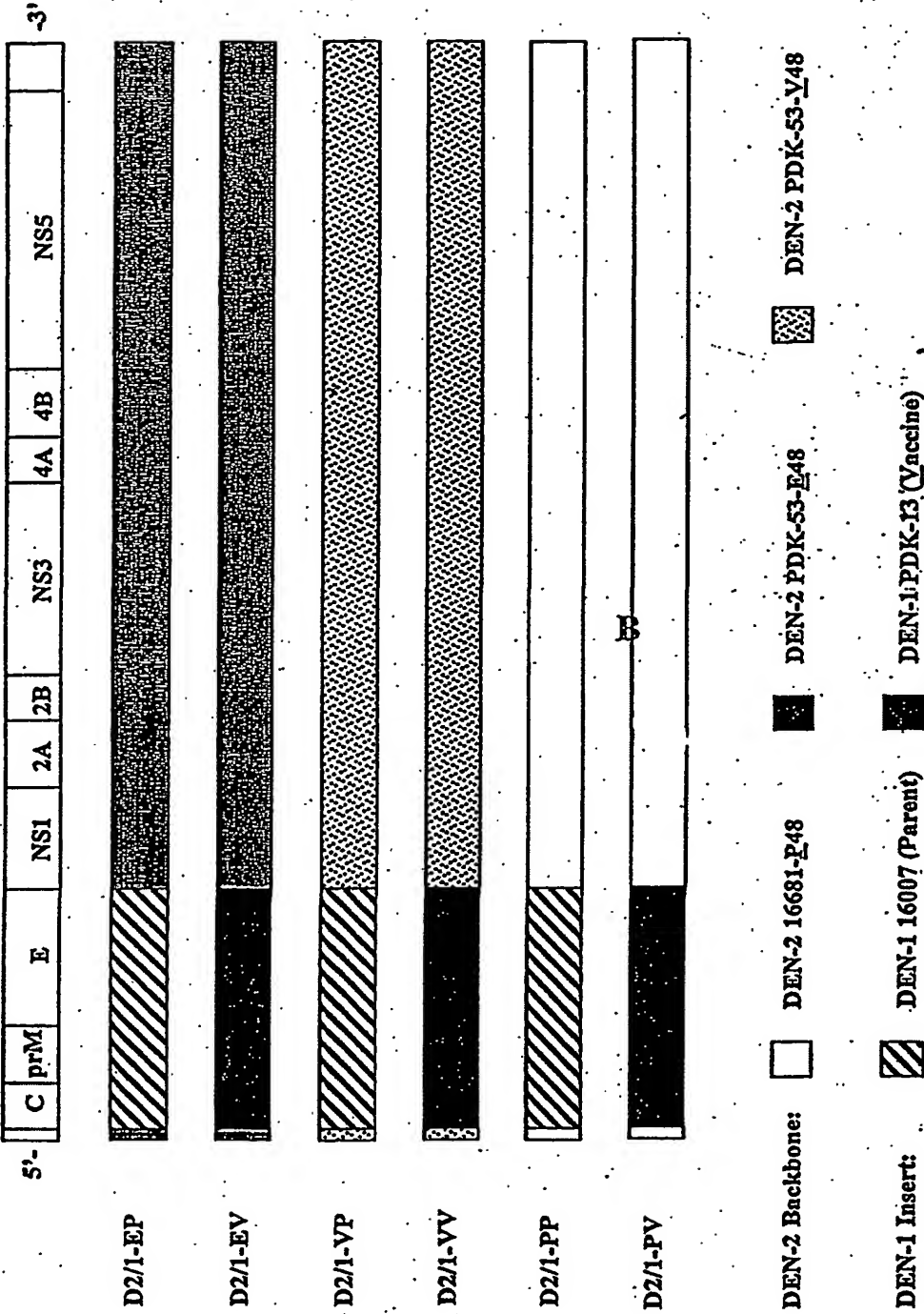
56. A nucleic acid chimera comprising the nucleotide sequence of claim 43 and a nucleotide sequence encoding a flavivirus structural protein selected from the group consisting of a C protein of dengue-1 virus, a prM protein of dengue-1 virus, an E protein of dengue-1 virus or any combination thereof.

57. A nucleic acid chimera comprising the nucleotide sequence of claim 43 and a nucleotide sequence encoding a flavivirus structural protein selected from the group consisting of a C protein of dengue-2 virus, a prM protein of dengue-2 virus, an E protein of dengue-2 virus or any combination thereof.

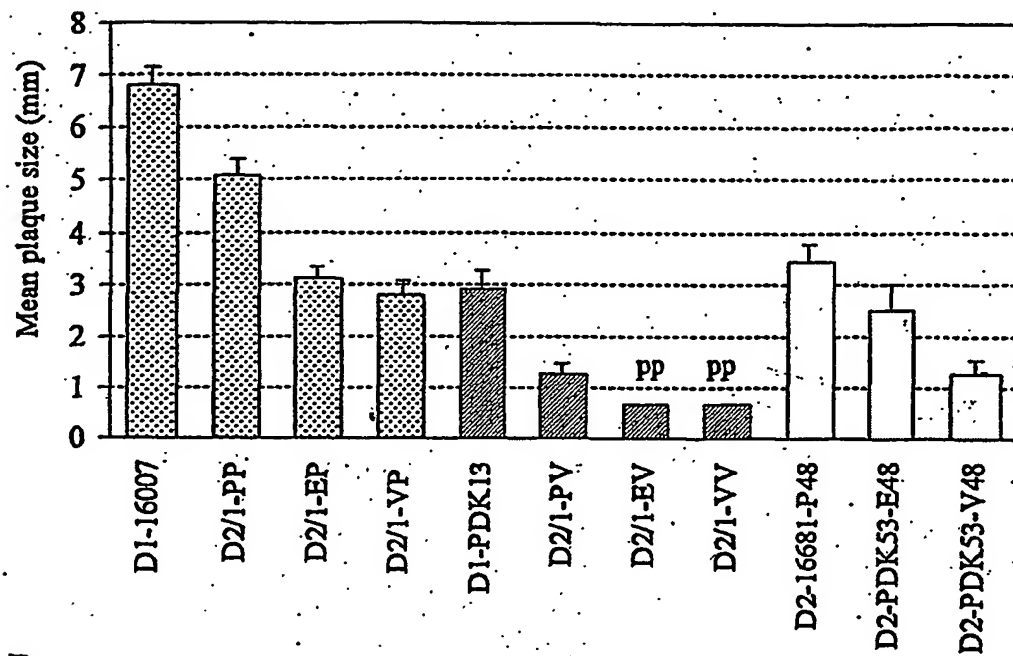
58. A nucleic acid chimera comprising the nucleotide sequence of claim 43 and a nucleotide sequence encoding a flavivirus structural protein selected from the group consisting of a C protein of dengue-3 virus, a prM protein of dengue-3 virus, an E protein of dengue-3 virus or any combination thereof.

59. A nucleic acid chimera comprising the nucleotide sequence of claim 43 and a nucleotide sequence encoding a flavivirus structural protein selected from the group consisting of a C protein of dengue-4 virus, a prM protein of dengue-4 virus, an E protein of dengue-4 virus or any combination thereof.

FIGURE 1



A



B

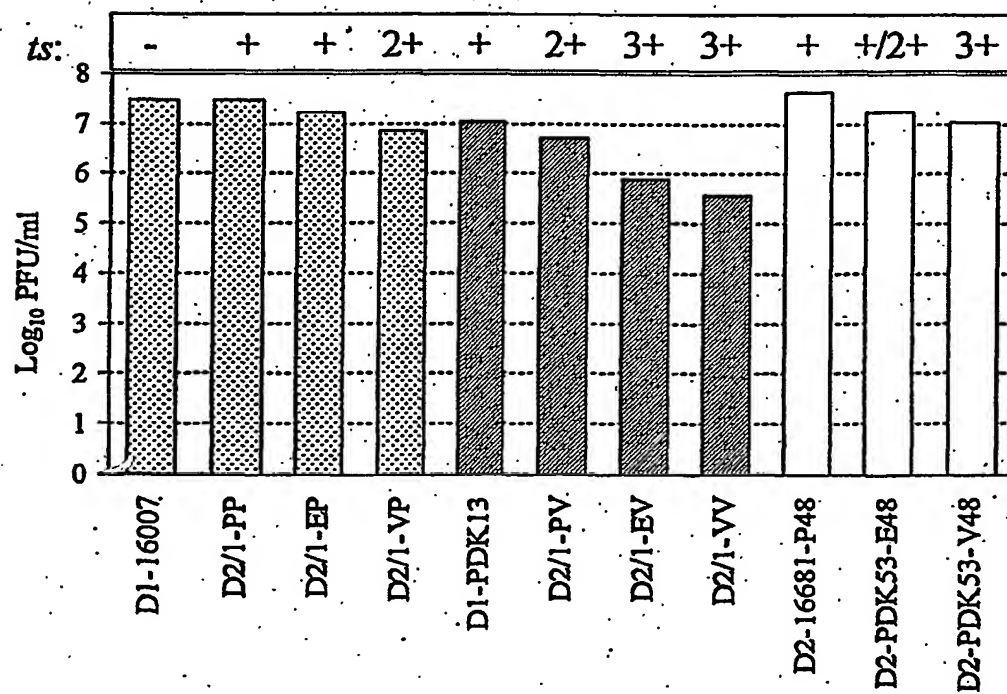


FIGURE 2

FIGURE 3

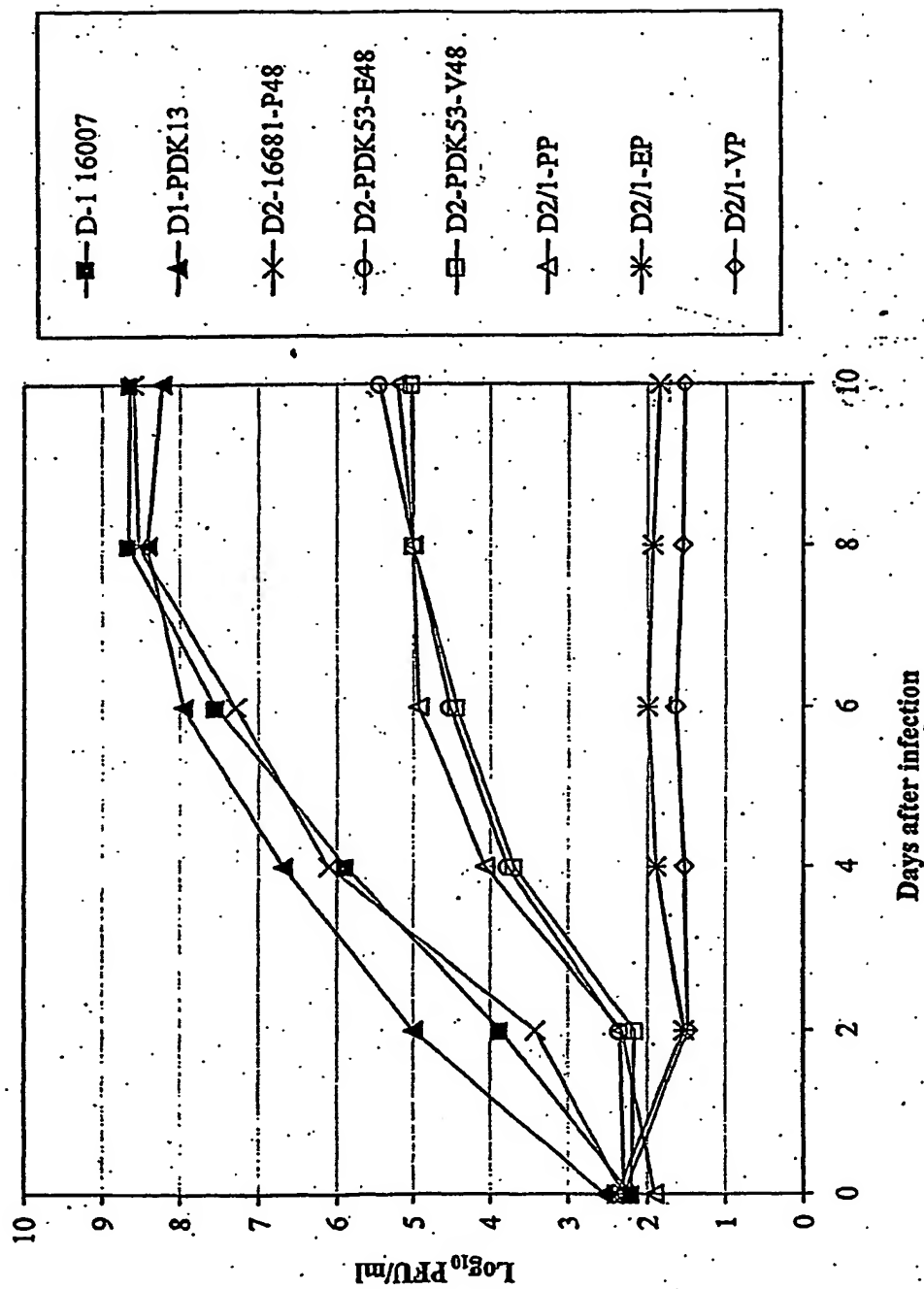


FIGURE 4

